

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Feder, John N.  
Kronmal, Gregory S.  
Lauer, Peter M.  
Ruddy, David A.  
Thomas, Winston  
Tsuchihashi, Zenta  
Wolff, Roger K.
- (ii) TITLE OF INVENTION: Megabase Transcript Map: Novel Sequences and Antibodies Thereto
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
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  - (C) CITY: San Francisco
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/724,394
  - (B) FILING DATE: 01-OCT-1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Fitts, Renee A.
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  - (C) REFERENCE/DOCKET NUMBER: 017957-000100
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  - (A) TELEPHONE: 415-576-0200
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## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 589 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Region
  - (B) LOCATION: 1..589
  - (D) OTHER INFORMATION: /note= "BT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Val	Phe	Pro	Ser	Ser	Gly	Leu	Pro	Arg	Cys	Leu	Xaa	Xaa	Xaa	1	5	10	15
Leu	Thr	Leu	Ile	Leu	Leu	Gln	Leu	Pro	Lys	Leu	Asp	Ser	Ala	Pro	Phe	20	25	30	
Asp	Val	Ile	Gly	Pro	Pro	Glu	Pro	Ile	Leu	Ala	Val	Val	Gly	Glu	Asp	35	40	45	
Ala	Glu	Leu	Pro	Cys	Arg	Leu	Ser	Pro	Asn	Ala	Ser	Ala	Glu	His	Leu	50	55	60	
Glu	Leu	Arg	Trp	Phe	Arg	Lys	Lys	Val	Ser	Pro	Ala	Val	Leu	Val	His	65	70	75	80
Arg	Asp	Gly	Arg	Glu	Gln	Glu	Ala	Glu	Gln	Met	Pro	Glu	Tyr	Arg	Gly	85	90	95	
Arg	Ala	Thr	Leu	Val	Gln	Asp	Gly	Ile	Ala	Lys	Gly	Arg	Val	Ala	Leu	100	105	110	
Arg	Ile	Arg	Gly	Val	Arg	Val	Ser	Asp	Asp	Gly	Glu	Tyr	Thr	Cys	Phe	115	120	125	
Phe	Arg	Glu	Asp	Gly	Ser	Tyr	Glu	Glu	Ala	Leu	Val	His	Leu	Lys	Val	130	135	140	
Ala	Ala	Leu	Gly	Ser	Asp	Pro	His	Ile	Ser	Met	Gln	Val	Gln	Glu	Asn	145	150	155	160
Gly	Glu	Ile	Cys	Leu	Glu	Cys	Thr	Ser	Val	Gly	Trp	Tyr	Pro	Glu	Pro	165	170	175	
Gln	Val	Gln	Trp	Arg	Thr	Ser	Lys	Gly	Glu	Lys	Phe	Pro	Ser	Thr	Ser	180	185	190	
Glu	Ser	Arg	Asn	Pro	Asp	Glu	Glu	Gly	Leu	Phe	Thr	Val	Ala	Ala	Ser	195	200	205	
Val	Ile	Ile	Arg	Asp	Thr	Ser	Thr	Lys	Asn	Val	Ser	Cys	Tyr	Ile	Gln	210	215	220	
Asn	Leu	Leu	Leu	Gly	Gln	Glu	Lys	Lys	Val	Glu	Ile	Ser	Ile	Pro	Ala	225	230	235	240
Ser	Ser	Leu	Pro	Arg	Leu	Thr	Pro	Trp	Ile	Val	Ala	Val	Ala	Val	Xaa	245	250	255	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Leu	Met	Val	260	265	270	
Leu	Gly	Leu	Leu	Thr	Ile	Gly	Ser	Ile	Phe	Phe	Thr	Trp	Arg	Leu	Tyr	275	280	285	
Asn	Glu	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Arg	Glu	Arg	Xaa	Xaa	290	295	300	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Asn	Glu	Phe	Ser	Xaa	Xaa	Xaa	305	310	315	320



Xaa Xaa Xaa Xaa Ser Lys Glu Arg Leu Leu Glu Glu Leu Lys Trp Lys  
 325 330 335  
 Lys Ala Thr Leu His Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 340 345 350  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Asp Val Thr Leu Asp Pro Asp  
 355 360 365  
 Thr Ala His Pro His Leu Phe Leu Tyr Glu Asp Ser Lys Ser Val Arg  
 370 375 380  
 Leu Glu Asp Ser Arg Gln Lys Xaa Xaa Xaa Leu Pro Glu Lys Thr Glu  
 385 390 395 400  
 Arg Phe Asp Ser Trp Pro Cys Val Leu Gly Arg Glu Thr Phe Thr Ser  
 405 410 415  
 Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Thr Asp Trp Ala  
 420 425 430  
 Ile Gly Val Cys Arg Glu Asn Val Met Lys Lys Xaa Gly Phe Asp Pro  
 435 440 445  
 Met Thr Pro Glu Asn Gly Phe Trp Ala Val Glu Leu Tyr Xaa Gly Asn  
 450 455 460  
 Gly Tyr Trp Ala Leu Thr Pro Leu Arg Thr Pro Leu Pro Leu Ala Gly  
 465 470 475 480  
 Pro Pro Arg Arg Val Gly Ile Phe Leu Asp Tyr Glu Ser Gly Asp Ile  
 485 490 495  
 Ser Phe Tyr Asn Met Asn Asp Gly Ser Asp Ile Tyr Thr Phe Ser Asn  
 500 505 510  
 Val Thr Phe Ser Gly Pro Leu Arg Phe Phe Phe Cys Leu Trp Ser Ser  
 515 520 525  
 Gly Lys Lys Pro Leu Thr Ile Cys Pro Ile Ala Asp Gly Pro Glu Arg  
 530 535 540  
 Val Thr Val Ile Ala Asn Ala Gln Asp Leu Ser Lys Glu Ile Pro Leu  
 545 550 555 560  
 Ser Pro Met Gly Glu Glu Ser Ala Pro Arg Asp Ala Asp Thr Leu His  
 565 570 575  
 Ser Lys Leu Ile Pro Thr Gln Pro Ser Gln Gly Ala Pro  
 580 585

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Region  
 (B) LOCATION: 1..581  
 (D) OTHER INFORMATION: /note= "BTF1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Glu Ser Ala Ala Ala Leu His Phe Ser Arg Pro Ala Ser Xaa Xaa
1           5           10           15

Xaa Xaa Leu Leu Leu Leu Leu Ser Leu Cys Ala Leu Val Ser Ala
20           25           30

Gln Phe Ile Val Val Gly Pro Thr Asp Pro Ile Leu Ala Thr Val Gly
35           40           45

Glu Asn Thr Thr Leu Arg Cys His Leu Ser Pro Glu Lys Asn Ala Glu
50           55           60

Asp Met Glu Val Arg Trp Phe Arg Ser Gln Phe Ser Pro Ala Val Phe
65           70           75           80

Val Tyr Lys Gly Gly Arg Glu Arg Thr Glu Glu Gln Met Glu Glu Tyr
85           90           95

Arg Gly Arg Thr Thr Phe Val Ser Lys Asp Ile Ser Arg Gly Ser Val
100          105          110

Ala Leu Val Ile His Asn Ile Thr Ala Gln Glu Asn Gly Thr Tyr Arg
115          120          125

Cys Tyr Phe Gln Glu Gly Arg Ser Tyr Asp Glu Ala Ile Leu His Leu
130          135          140

Val Val Ala Gly Leu Gly Ser Lys Pro Leu Ile Ser Met Arg Gly His
145          150          155          160

Glu Asp Gly Gly Ile Arg Leu Glu Cys Ile Ser Arg Gly Trp Tyr Pro
165          170          175

Lys Pro Leu Thr Val Trp Arg Asp Pro Tyr Gly Gly Val Ala Pro Ala
180          185          190

Leu Lys Glu Val Ser Met Pro Asp Ala Asp Gly Leu Phe Met Val Thr
195          200          205

Thr Ala Val Ile Ile Arg Asp Lys Ser Val Arg Asn Met Ser Cys Ser
210          215          220

Ile Asn Asn Thr Leu Leu Gly Gln Lys Lys Glu Ser Val Ile Phe Ile
225          230          235          240

Pro Glu Ser Phe Met Pro Ser Val Ser Pro Cys Ala Val Ala Leu Pro
245          250          255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Ile Val
260          265          270

Val Ile Leu Met Ile Pro Ile Ala Val Cys Ile Tyr Trp Ile Asn Lys
275          280          285

```

Leu Gln Lys Glu Lys Lys Ile Leu Ser Gly Glu Lys Glu Phe Glu Arg  
 290 295 300  
 Glu Thr Arg Glu Ile Ala Leu Lys Glu Leu Glu Lys Glu Arg Val Gln  
 305 310 315 320  
 Lys Glu Glu Glu Leu Gln Val Lys Glu Lys Leu Gln Glu Glu Leu Arg  
 325 330 335  
 Trp Arg Arg Thr Phe Leu His Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 340 345 350  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Asp Val Val Leu Asp  
 355 360 365  
 Pro Asp Thr Ala His Pro Asp Leu Phe Leu Ser Glu Asp Arg Arg Ser  
 370 375 380  
 Val Arg Arg Cys Pro Phe Arg His Leu Gly Glu Ser Val Pro Asp Asn  
 385 390 395 400  
 Pro Glu Arg Phe Asp Ser Gln Pro Cys Val Leu Gly Arg Glu Ser Phe  
 405 410 415  
 Ala Ser Gly Lys His Tyr Trp Glu Val Glu Val Glu Asn Val Ile Glu  
 420 425 430  
 Trp Thr Val Gly Val Cys Arg Asp Ser Val Glu Arg Lys Xaa Gly Glu  
 435 440 445  
 Val Leu Leu Ile Pro Gln Asn Gly Phe Trp Thr Leu Glu Met His Xaa  
 450 455 460  
 Lys Gly Gln Tyr Arg Ala Val Ser Ser Pro Asp Arg Ile Leu Pro Leu  
 465 470 475 480  
 Lys Glu Ser Leu Cys Arg Val Gly Val Phe Leu Asp Tyr Glu Ala Gly  
 485 490 495  
 Asp Val Ser Phe Tyr Asn Met Arg Asp Arg Ser His Ile Tyr Thr Cys  
 500 505 510  
 Pro Arg Ser Ala Phe Ser Val Pro Val Arg Phe Phe Phe Arg Leu Gly  
 515 520 525  
 Cys Xaa Glu Asp Ser Pro Ile Phe Ile Cys Pro Ala Leu Thr Gly Ala  
 530 535 540  
 Asn Gly Val Thr Val Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 545 550 555 560  
 Xaa Xaa Xaa Xaa Xaa Xaa Glu Glu Gly Leu Thr Leu His Arg Val Gly  
 565 570 575  
 Thr His Gln Ser Leu  
 580

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 581 amino acids  
 (B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Region  
 (B) LOCATION: 1..581  
 (D) OTHER INFORMATION: /note= "BTF2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met Glu Pro Ala Ala Ala Leu His Phe Ser Leu Pro Ala Ser Leu Leu
1          5          10          15
Leu Leu Leu Leu Leu Leu Leu Ser Leu Cys Ala Leu Val Ser Ala
20          25          30
Gln Phe Thr Val Val Gly Pro Ala Asn Pro Ile Leu Ala Met Val Gly
35          40          45
Glu Asn Thr Thr Leu Arg Cys His Leu Ser Pro Glu Lys Asn Ala Glu
50          55          60
Asp Met Glu Val Arg Trp Phe Arg Ser Gln Phe Ser Pro Ala Val Phe
65          70          75          80
Val Tyr Lys Gly Gly Arg Glu Arg Thr Glu Glu Gln Met Glu Glu Tyr
85          90          95
Arg Gly Arg Ile Thr Phe Val Ser Lys Asp Ile Asn Arg Gly Ser Val
100         105         110
Ala Leu Val Ile His Asn Val Thr Ala Gln Glu Asn Gly Ile Tyr Arg
115         120         125
Cys Tyr Phe Gln Glu Gly Arg Ser Tyr Asp Glu Ala Ile Leu Arg Leu
130         135         140
Val Val Ala Gly Leu Gly Ser Lys Pro Leu Ile Glu Ile Lys Ala Gln
145         150         155         160
Glu Asp Gly Ser Ile Trp Leu Glu Cys Ile Ser Gly Gly Trp Tyr Pro
165         170         175
Glu Pro Leu Thr Val Trp Arg Asp Pro Tyr Gly Glu Val Val Pro Ala
180         185         190
Leu Lys Glu Val Ser Ile Ala Asp Ala Asp Gly Leu Phe Met Val Thr
195         200         205
Thr Ala Val Ile Ile Arg Asp Lys Tyr Val Arg Asn Val Ser Cys Ser
210         215         220
Val Asn Asn Thr Leu Leu Gly Gln Glu Lys Glu Thr Val Ile Phe Ile
225         230         235         240
Pro Glu Ser Phe Met Pro Ser Ala Ser Pro Trp Met Val Ala Leu Ala
245         250         255

```

Val Ile Leu Thr Ala Ser Pro Trp Met Val Ser Met Thr Val Ile Leu  
 260 265 270  
 Ala Val Phe Ile Ile Phe Met Ala Val Ser Ile Cys Cys Ile Lys Lys  
 275 280 285  
 Leu Gln Arg Glu Lys Lys Ile Leu Ser Gly Glu Lys Lys Val Glu Gln  
 290 295 300  
 Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Lys Glu Xaa Xaa Xaa  
 305 310 315 320  
 Xaa Xaa Xaa Xaa Xaa Xaa Ile Ala Gln Gln Leu Gln Glu Glu Leu Arg  
 325 330 335  
 Trp Arg Arg Thr Phe Leu His Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 340 345 350  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Asp Val Val Leu Asp  
 355 360 365  
 Pro Asp Thr Ala His Pro Glu Leu Phe Leu Ser Glu Asp Arg Arg Ser  
 370 375 380  
 Val Arg Arg Gly Pro Tyr Arg Gln Arg Xaa Xaa Xaa Val Pro Asp Asn  
 385 390 395 400  
 Pro Glu Arg Phe Asp Ser Gln Pro Cys Val Leu Gly Trp Glu Ser Phe  
 405 410 415  
 Ala Ser Gly Lys His Tyr Trp Glu Val Glu Val Glu Asn Val Met Val  
 420 425 430  
 Trp Thr Val Gly Val Cys Arg His Ser Val Glu Arg Lys Xaa Gly Glu  
 435 440 445  
 Val Leu Leu Ile Pro Gln Asn Gly Phe Trp Thr Leu Glu Met Phe Xaa  
 450 455 460  
 Gly Asn Gln Tyr Arg Ala Leu Ser Ser Pro Glu Arg Ile Leu Pro Leu  
 465 470 475 480  
 Lys Glu Ser Leu Cys Arg Val Gly Val Phe Leu Asp Tyr Glu Ala Gly  
 485 490 495  
 Asp Val Ser Phe Tyr Asn Met Arg Asp Arg Ser His Ile Tyr Thr Cys  
 500 505 510  
 Pro Arg Ser Ala Phe Thr Val Pro Val Arg Phe Phe Phe Arg Leu Gly  
 515 520 525  
 Ser Xaa Asp Asp Ser Pro Ile Phe Ile Cys Pro Ala Leu Thr Gly Ala  
 530 535 540  
 Ser Gly Val Met Val Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 545 550 555 560  
 Xaa Xaa Xaa Xaa Xaa Xaa Glu Glu Gly Leu Lys Leu His Arg Val Gly  
 565 570 575  
 Thr His Gln Ser Leu  
 580

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..540
- (D) OTHER INFORMATION: /note= "BTF5"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Lys Met Ala Ser Phe Leu Ala Phe Leu Leu Leu Asn Phe Arg Xaa
 1             5             10             15

Xaa Xaa Val Cys Leu Leu Leu Leu Gln Leu Leu Met Pro His Ser Ala
 20             25             30

Gln Phe Ser Val Leu Gly Pro Ser Gly Pro Ile Leu Ala Met Val Gly
 35             40             45

Glu Asp Ala Asp Leu Pro Cys His Leu Phe Pro Thr Met Ser Ala Glu
 50             55             60

Thr Met Glu Leu Lys Trp Val Ser Ser Ser Leu Arg Gln Val Val Asn
 65             70             75             80

Val Tyr Ala Asp Gly Lys Glu Val Glu Asp Arg Gln Ser Ala Pro Tyr
 85             90             95

Arg Gly Arg Thr Ser Ile Leu Arg Asp Gly Ile Thr Ala Gly Lys Ala
100            105            110

Ala Leu Arg Ile His Asn Val Thr Ala Ser Asp Ser Gly Lys Tyr Leu
115            120            125

Cys Tyr Phe Gln Asp Gly Asp Phe Tyr Glu Lys Ala Leu Val Glu Leu
130            135            140

Lys Val Ala Ala Leu Gly Ser Asp Leu His Val Asp Val Lys Gly Tyr
145            150            155            160

Lys Asp Gly Gly Ile His Leu Glu Cys Arg Ser Thr Gly Trp Tyr Pro
165            170            175

Gln Pro Gln Ile Gln Trp Ser Asn Asn Lys Gly Glu Asn Ile Pro Thr
180            185            190

Val Glu Ala Pro Val Val Ala Asp Gly Val Gly Leu Tyr Ala Val Ala
195            200            205

Ala Ser Val Ile Met Arg Gly Ser Ser Gly Glu Gly Val Ser Cys Thr
210            215            220

Ile Arg Ser Ser Leu Leu Gly Leu Glu Lys Thr Ala Ser Ile Ser Ile

```

225		230		235		240
Ala Asp Pro Phe	Phe Arg Ser Ala Gln Arg Trp Ile Ala Ala Leu Ala					
	245		250		255	
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Leu						
	260		265		270	
Pro Val Leu Leu Leu Leu Leu Gly Gly Ala Gly Tyr Phe Leu Trp Gln						
	275		280		285	
Gln Gln Glu Glu Lys Lys Thr Gln Phe Arg Lys Lys Lys Arg Glu Gln						
	290		295		300	
Glu Leu Arg Glu Met Ala Trp Ser Thr Met Lys Gln Glu Gln Ser Xaa						
	305		310		315	320
Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Val Lys Leu Leu Glu Glu Leu Arg						
	325		330		335	
Trp Arg Ser Ile Gln Tyr Ala Ser Arg Gly Glu Arg His Ser Ala Tyr						
	340		345		350	
Asn Glu Trp Lys Lys Ala Leu Phe Lys Pro Ala Asp Val Ile Leu Asp						
	355		360		365	
Pro Lys Thr Ala Asn Pro Ile Leu Leu Val Ser Glu Asp Gln Arg Ser						
	370		375		380	
Val Gln Arg Ala Lys Glu Pro Gln Asp Xaa Xaa Xaa Leu Pro Asp Asn						
	385		390		395	400
Pro Glu Arg Phe Asn Trp His Tyr Cys Val Leu Gly Cys Glu Ser Phe						
	405		410		415	
Ile Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Lys Glu						
	420		425		430	
Trp His Ile Gly Val Cys Ser Lys Asn Val Gln Arg Lys Xaa Gly Trp						
	435		440		445	
Val Lys Met Thr Pro Glu Asn Gly Phe Trp Thr Met Gly Leu Thr Asp						
	450		455		460	
Gly Asn Lys Tyr Arg Thr Leu Thr Glu Pro Arg Thr Asn Leu Lys Leu						
	465		470		475	480
Pro Lys Pro Pro Lys Lys Val Gly Val Phe Leu Asp Tyr Glu Thr Gly						
	485		490		495	
Asp Ile Ser Phe Tyr Asn Ala Val Asp Gly Ser His Ile His Thr Phe						
	500		505		510	
Leu Asp Val Ser Phe Ser Glu Ala Leu Tyr Phe Val Phe Arg Ile Leu						
	515		520		525	
Thr Leu Glu Pro Thr Ala Leu Ser Ile Cys Pro Ala						
	530		535		540	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..610
- (D) OTHER INFORMATION: /note= "BTF3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Lys	Met	Ala	Ser	Ser	Leu	Ala	Phe	Leu	Leu	Leu	Asn	Phe	His	Xaa	1	5	10	15
Xaa	Xaa	Val	Ser	Leu	Phe	Leu	Val	Gln	Leu	Leu	Thr	Pro	Cys	Ser	Ala	20	25	30	
Gln	Phe	Ser	Val	Leu	Gly	Pro	Ser	Gly	Pro	Ile	Leu	Ala	Met	Val	Gly	35	40	45	
Glu	Asp	Ala	Asp	Leu	Pro	Cys	His	Leu	Phe	Pro	Thr	Met	Ser	Ala	Glu	50	55	60	
Thr	Met	Glu	Leu	Arg	Trp	Val	Ser	Ser	Ser	Leu	Arg	Gln	Val	Val	Asn	65	70	75	80
Val	Tyr	Ala	Asp	Gly	Lys	Glu	Val	Glu	Asp	Arg	Gln	Ser	Ala	Pro	Tyr	85	90	95	
Arg	Gly	Arg	Thr	Ser	Ile	Leu	Arg	Asp	Gly	Ile	Thr	Ala	Gly	Lys	Ala	100	105	110	
Ala	Leu	Arg	Ile	His	Asn	Val	Thr	Ala	Ser	Asp	Ser	Gly	Lys	Tyr	Leu	115	120	125	
Cys	Tyr	Phe	Gln	Asp	Gly	Asp	Phe	Tyr	Glu	Lys	Ala	Leu	Val	Glu	Leu	130	135	140	
Lys	Val	Ala	Ala	Leu	Gly	Ser	Asp	Leu	His	Ile	Glu	Val	Lys	Gly	Tyr	145	150	155	160
Glu	Asp	Gly	Gly	Ile	His	Leu	Glu	Cys	Arg	Ser	Thr	Gly	Trp	Tyr	Pro	165	170	175	
Gln	Pro	Gln	Ile	Lys	Trp	Ser	Asp	Thr	Lys	Gly	Glu	Asn	Ile	Pro	Ala	180	185	190	
Val	Glu	Ala	Pro	Val	Val	Ala	Asp	Gly	Val	Gly	Leu	Tyr	Ala	Val	Ala	195	200	205	
Ala	Ser	Val	Ile	Met	Arg	Gly	Ser	Ser	Gly	Gly	Gly	Val	Ser	Cys	Ile	210	215	220	
Ile	Arg	Asn	Ser	Leu	Leu	Gly	Leu	Glu	Lys	Thr	Ala	Ser	Ile	Ser	Ile	225	230	235	240
Ala	Asp	Pro	Phe	Phe	Arg	Ser	Ala	Gln	Pro	Trp	Ile	Ala	Ala	Leu	Ala				



245250255

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Leu  
260265270

Pro Ile Ser Leu Leu Leu Leu Ala Gly Ala Ser Tyr Phe Leu Trp Arg  
275280285

Gln Gln Lys Glu Lys Ile Ala Leu Ser Arg Glu Thr Glu Arg Glu Arg  
290295300

Glu Met Lys Glu Met Gly Tyr Ala Ala Thr Glu Gln Glu Ile Ser Xaa  
305310315320

Xaa Xaa Xaa Xaa Xaa Xaa Leu Arg Glu Lys Leu Gln Glu Glu Leu Lys  
325330335

Trp Arg Lys Ile Gln Tyr Met Ala Arg Gly Glu Lys Ser Leu Ala Tyr  
340345350

His Glu Trp Lys Met Ala Leu Phe Lys Pro Ala Asp Val Ile Leu Asp  
355360365

Pro Asp Thr Ala Asn Ala Ile Leu Leu Val Ser Glu Asp Gln Arg Ser  
370375380

Val Gln Arg Ala Glu Glu Pro Arg Asp Xaa Xaa Xaa Leu Pro Asp Asn  
385390395400

Pro Glu Arg Phe Glu Trp Arg Tyr Cys Val Leu Gly Cys Glu Asn Phe  
405410415

Thr Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Lys Glu  
420425430

Trp His Ile Gly Val Cys Ser Lys Asn Val Glu Arg Lys Lys Gly Trp  
435440445

Val Lys Met Thr Pro Glu Asn Gly Tyr Trp Thr Met Gly Leu Thr Asp  
450455460

Gly Asn Lys Tyr Arg Ala Leu Thr Glu Pro Arg Thr Asn Leu Lys Leu  
465470475480

Pro Glu Pro Pro Arg Lys Val Gly Ile Phe Leu Asp Tyr Glu Thr Gly  
485490495

Glu Ile Ser Phe Tyr Asn Ala Thr Asp Gly Ser His Ile Tyr Thr Phe  
500505510

Pro His Ala Ser Phe Ser Glu Pro Leu Tyr Phe Val Phe Arg Ile Leu  
515520525

Thr Leu Glu Pro Thr Ala Leu Thr Ile Cys Pro Ile Pro Lys Glu Val  
530535540

Glu Ser Ser Pro Asp Pro Asp Leu Val Pro Asp His Ser Leu Glu Thr  
545550555560

Pro Leu Thr Pro Gly Leu Ala Asn Glu Ser Gly Glu Pro Gln Ala Glu  
565570575

Val Thr Ser Leu Leu Leu Pro Ala His Pro Gly Ala Glu Val Ser Pro  
                   580                  585                  590

Ser Ala Thr Thr Asn Gln Asn His Lys Leu Gln Ala Arg Thr Glu Ala  
                   595                  600                  605

Leu Tyr  
       610

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: /note= "BTF4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Xaa  
 1                  5                  10                  15

Xaa Xaa Val Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala  
                   20                  25                  30

Gln Phe Ser Val Leu Gly Pro Ser Gly Pro Ile Leu Ala Met Val Gly  
                   35                  40                  45

Glu Asp Ala Asp Leu Pro Cys His Leu Phe Pro Thr Met Ser Ala Glu  
                   50                  55                  60

Thr Met Glu Leu Lys Trp Val Ser Ser Ser Leu Arg Gln Val Val Asn  
                   65                  70                  75                  80

Val Tyr Ala Asp Gly Lys Glu Val Glu Asp Arg Gln Ser Ala Pro Tyr  
                   85                  90                  95

Arg Gly Arg Thr Ser Ile Leu Arg Asp Gly Ile Thr Ala Gly Lys Ala  
                   100                  105                  110

Ala Leu Arg Ile His Asn Val Thr Ala Ser Asp Ser Gly Lys Tyr Leu  
                   115                  120                  125

Cys Tyr Phe Gln Asp Gly Asp Phe Tyr Glu Lys Ala Leu Val Glu Leu  
                   130                  135                  140

Lys Val Ala Ala Leu Gly Ser Asn Leu His Val Glu Val Lys Gly Tyr  
                   145                  150                  155                  160

Glu Asp Gly Gly Ile His Leu Glu Cys Arg Ser Thr Gly Trp Tyr Pro  
                   165                  170                  175

Gln Pro Gln Ile Gln Trp Ser Asn Ala Lys Gly Glu Asn Ile Pro Ala

180	185	190
Val Glu Ala Pro Val Val Ala Asp Gly Val Gly Leu Tyr Glu Val Ala		
195	200	205
Ala Ser Val Ile Met Arg Gly Gly Ser Gly Glu Gly Val Ser Cys Ile		
210	215	220
Ile Arg Asn Ser Leu Leu Gly Leu Glu Lys Thr Ala Ser Ile Ser Ile		
225	230	235
Ala Asp Pro Phe Phe Arg Ser Ala Gln Pro Trp Ile Ala Ala Leu Ala		
245	250	255
Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Leu		
260	265	270
Pro Ile Leu Leu Leu Leu Leu Ala Gly Ala Ser Tyr Phe Leu Trp Arg		
275	280	285
Gln Gln Lys Glu Ile Thr Ala Leu Ser Ser Glu Ile Glu Ser Glu Gln		
290	295	300
Glu Met Lys Glu Met Gly Tyr Ala Ala Thr Glu Arg Glu Ile Ser Xaa		
305	310	315
Xaa Xaa Xaa Xaa Xaa Xaa Leu Arg Glu Ser Leu Gln Glu Glu Leu Lys		
325	330	335
Arg Lys Lys Ser Ser Thr		
340		

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: /note= "52 kD Ro"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Ser	Ala	Ala	Arg	Leu	Thr	Met	Met	Trp	Glu	Glu	Val	Thr	Cys
1				5					10					15	
Pro	Ile	Cys	Leu	Asp	Pro	Phe	Val	Glu	Pro	Val	Ser	Ile	Glu	Cys	Gly
			20					25					30		
His	Ser	Phe	Cys	Gln	Glu	Cys	Ile	Ser	Gln	Val	Gly	Lys	Gly	Gly	Gly
		35				40					45				
Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Cys	Pro	Val	Cys	Arg	Gln
50						55					60				

Arg	Phe	Leu	Leu	Lys	Asn	Leu	Arg	Pro	Asn	Arg	Gln	Leu	Ala	Asn	Met	65	70	75	80
Val	Asn	Asn	Leu	Lys	Glu	Ile	Ser	Gln	Glu	Ala	Arg	Glu	Gly	Thr	Gln	85	90	95	
Gly	Glu	Arg	Cys	Ala	Val	His	Gly	Glu	Arg	Leu	His	Leu	Phe	Cys	Glu	100	105	110	
Lys	Asp	Gly	Lys	Ala	Leu	Cys	Trp	Val	Cys	Ala	Gln	Ser	Arg	Lys	His	115	120	125	
Arg	Asp	His	Ala	Met	Val	Pro	Leu	Glu	Glu	Ala	Ala	Gln	Glu	Tyr	Gln	130	135	140	
Glu	Lys	Leu	Gln	Val	Ala	Leu	Gly	Glu	Leu	Arg	Arg	Lys	Gln	Glu	Leu	145	150	155	160
Ala	Glu	Lys	Leu	Glu	Val	Glu	Ile	Ala	Ile	Lys	Arg	Ala	Asp	Trp	Lys	165	170	175	
Lys	Thr	Val	Glu	Thr	Gln	Lys	Ser	Arg	Ile	His	Ala	Glu	Phe	Val	Gln	180	185	190	
Gln	Lys	Asn	Phe	Leu	Val	Glu	Glu	Glu	Gln	Arg	Gln	Leu	Gln	Glu	Leu	195	200	205	
Glu	Lys	Asp	Glu	Arg	Glu	Gln	Leu	Arg	Ile	Leu	Gly	Glu	Lys	Glu	Ala	210	215	220	
Lys	Leu	Ala	Gln	Gln	Ser	Gln	Ala	Leu	Gln	Glu	Leu	Ile	Ser	Glu	Leu	225	230	235	240
Asp	Arg	Arg	Cys	His	Ser	Ser	Ala	Leu	Glu	Leu	Leu	Gln	Glu	Val	Ile	245	250	255	
Ile	Val	Leu	Glu	Arg	Ser	Glu	Ser	Trp	Asn	Leu	Lys	Asp	Leu	Asp	Ile	260	265	270	
Thr	Ser	Pro	Glu	Leu	Arg	Ser	Val	Cys	His	Val	Pro	Xaa	Xaa	Xaa	Xaa	275	280	285	
Gly	Leu	Lys	Lys	Met	Leu	Arg	Thr	Cys	Ala	Val	His	Ile	Thr	Leu	Asp	290	295	300	
Pro	Asp	Thr	Ala	Asn	Pro	Trp	Leu	Ile	Leu	Ser	Glu	Asp	Arg	Arg	Gln	305	310	315	320
Val	Arg	Leu	Gly	Asp	Thr	Gln	Gln	Ser	Ile	Pro	Gly	Asn	Glu	Glu	Arg	325	330	335	
Phe	Asp	Ser	Tyr	Pro	Met	Val	Leu	Gly	Ala	Gln	His	Phe	His	Ser	Gly	340	345	350	
Lys	His	Tyr	Trp	Glu	Val	Asp	Val	Thr	Gly	Lys	Glu	Ala	Trp	Asp	Leu	355	360	365	
Gly	Val	Cys	Arg	Asp	Ser	Val	Arg	Arg	Lys	Gly	His	Phe	Leu	Leu	Ser	370	375	380	
Ser	Lys	Ser	Gly	Phe	Trp	Thr	Ile	Trp	Leu	Trp	Asn	Lys	Gln	Lys	Tyr	385	390	395	400

Glu	Ala	Gly	Thr	Tyr 405	Pro	Gln	Thr	Pro	Leu	His	Leu	Gln	Val	Pro	Pro
Cys	Gln	Val	Gly 420	Ile	Phe	Leu	Asp	Tyr 425	Glu	Ala	Gly	Met	Val 430	Ser	Phe
Tyr	Asn	Ile 435	Thr	Asp	His	Gly	Ser 440	Leu	Ile	Tyr	Ser	Phe 445	Ser	Glu	Cys
Ala 450	Phe	Thr	Gly	Pro	Leu	Arg 455	Pro	Phe	Phe	Ser	Pro 460	Gly	Phe	Asn	Asp
Gly 465	Gly	Lys	Asn	Thr 470	Ala	Pro	Leu	Thr	Leu	Cys 475	Pro	Leu	Asn	Ile	Gly 480
Ser	Gln	Gly	Ser 485	Thr	Asp	Tyr									

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Region  
(B) LOCATION: 1..485  
(D) OTHER INFORMATION: /note= "RoRet"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met 1	Ala	Ser	Thr 5	Thr	Ser	Thr	Lys	Lys	Met 10	Met	Glu	Glu	Ala	Thr 15	Cys
Ser	Ile	Cys	Leu 20	Ser	Leu	Met	Thr	Asn 25	Pro	Val	Ser	Ile	Asn 30	Cys	Gly
His	Ser	Tyr 35	Cys	His	Leu	Cys	Ile 40	Thr	Asp	Phe	Phe	Lys 45	Asn	Pro	Ser
Gln	Lys 50	Gln	Leu	Arg	Gln	Glu 55	Thr	Phe	Cys	Cys	Pro 60	Gln	Cys	Arg	Ala
Pro 65	Phe	His	Met	Asp	Ser 70	Leu	Arg	Pro	Asn	Lys 75	Gln	Leu	Gly	Ser	Leu 80
Ile	Glu	Ala	Leu	Lys 85	Glu	Thr	Asp	Gln	Glu 90	Met	Xaa	Xaa	Xaa 95	Xaa	Xaa
Xaa	Xaa	Ser	Cys 100	Glu	Glu	His	Gly	Glu 105	Gln	Phe	His	Leu	Phe 110	Cys	Glu
Asp	Glu	Gly 115	Gln	Leu	Ile	Cys	Trp 120	Arg	Cys	Glu	Arg	Ala 125	Pro	Gln	His
Lys	Gly	His	Thr	Thr	Ala	Leu	Val	Glu	Asp	Val	Cys	Gln	Gly	Tyr	Lys

130					135					140					
Glu	Lys	Leu	Gln	Lys	Ala	Val	Thr	Lys	Leu	Lys	Gln	Leu	Glu	Asp	Arg
145					150					155					160
Cys	Thr	Glu	Gln	Lys	Leu	Ser	Thr	Ala	Met	Arg	Ile	Thr	Lys	Trp	Lys
				165					170					175	
Glu	Lys	Val	Gln	Ile	Gln	Arg	Gln	Lys	Ile	Arg	Ser	Asp	Phe	Lys	Asn
			180					185					190		
Leu	Gln	Cys	Phe	Leu	His	Glu	Glu	Glu	Lys	Ser	Tyr	Leu	Trp	Arg	Leu
		195					200					205			
Glu	Lys	Glu	Glu	Gln	Gln	Thr	Leu	Ser	Arg	Leu	Arg	Asp	Tyr	Glu	Ala
		210				215					220				
Gly	Leu	Gly	Leu	Lys	Ser	Asn	Glu	Leu	Lys	Ser	His	Ile	Leu	Glu	Leu
225					230					235					240
Glu	Glu	Lys	Cys	Gln	Gly	Ser	Ala	Gln	Lys	Leu	Leu	Gln	Asn	Val	Asn
				245					250					255	
Asp	Thr	Leu	Ser	Arg	Ser	Trp	Ala	Val	Lys	Leu	Glu	Thr	Ser	Glu	Ala
			260					265					270		
Val	Ser	Leu	Glu	Leu	His	Thr	Met	Cys	Asn	Val	Ser	Lys	Leu	Tyr	Phe
		275					280					285			
Asp	Val	Lys	Lys	Met	Leu	Arg	Ser	His	Gln	Val	Ser	Val	Thr	Leu	Asp
	290					295					300				
Pro	Asp	Thr	Ala	His	His	Glu	Leu	Ile	Leu	Ser	Glu	Asp	Arg	Arg	Gln
305					310					315					320
Val	Thr	Arg	Gly	Tyr	Thr	Gln	Glu	Asn	Gln	Asp	Thr	Ser	Ser	Arg	Arg
			325						330					335	
Phe	Thr	Ala	Phe	Pro	Cys	Val	Leu	Gly	Cys	Glu	Gly	Phe	Thr	Ser	Gly
			340					345					350		
Arg	Arg	Tyr	Phe	Glu	Val	Asp	Val	Gly	Glu	Gly	Thr	Gly	Trp	Asp	Leu
		355					360					365			
Gly	Val	Cys	Met	Glu	Asn	Val	Gln	Arg	Gly	Thr	Gly	Met	Lys	Gln	Glu
	370					375					380				
Pro	Gln	Ser	Gly	Phe	Trp	Thr	Leu	Arg	Leu	Cys	Lys	Lys	Lys	Gly	Tyr
385					390					395					400
Val	Ala	Leu	Thr	Ser	Pro	Pro	Thr	Ser	Leu	His	Leu	His	Glu	Gln	Pro
				405					410					415	
Leu	Leu	Val	Gly	Ile	Phe	Leu	Asp	Tyr	Glu	Ala	Gly	Val	Val	Ser	Phe
			420					425					430		
Tyr	Asn	Gly	Xaa	Asn	Thr	Gly	Cys	His	Ile	Phe	Thr	Phe	Pro	Lys	Ala
		435					440					445			
Ser	Phe	Ser	Asp	Thr	Leu	Arg	Pro	Tyr	Phe	Gln	Val	Tyr	Gln	Tyr	Ser
						455					460				

Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Phe Leu Pro Pro Pro Xaa Xaa Gly  
 465 470 475 480

Xaa Xaa Xaa Xaa Asp  
 485

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: /note= "NPT1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Gln	Met	Asp	Asn	Arg	Leu	Pro	Pro	Lys	Lys	Val	Pro	Gly	Phe	Cys	1	5	10	15
Ser	Phe	Arg	Tyr	Gly	Leu	Ser	Phe	Leu	Val	His	Cys	Cys	Asn	Val	Ile	20	25	30	
Ile	Thr	Ala	Gln	Arg	Ala	Cys	Leu	Asn	Leu	Thr	Met	Val	Val	Met	Val	35	40	45	
Asn	Ser	Thr	Asp	Pro	His	Gly	Leu	Pro	Asn	Thr	Ser	Thr	Lys	Lys	Leu	50	55	60	
Leu	Asp	Asn	Ile	Lys	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	65	70	75	80
Xaa	Xaa	Xaa	Pro	Met	Tyr	Asn	Trp	Ser	Pro	Asp	Ile	Gln	Gly	Ile	Ile	85	90	95	
Leu	Ser	Ser	Thr	Ser	Tyr	Gly	Val	Ile	Ile	Ile	Gln	Val	Pro	Val	Gly	100	105	110	
Tyr	Phe	Ser	Gly	Ile	Tyr	Ser	Thr	Lys	Lys	Met	Ile	Gly	Phe	Ala	Leu	115	120	125	
Cys	Leu	Ser	Ser	Val	Leu	Ser	Leu	Leu	Ile	Pro	Pro	Ala	Ala	Gly	Ile	130	135	140	
Gly	Val	Ala	Trp	Val	Val	Val	Cys	Arg	Ala	Val	Gln	Gly	Ala	Ala	Gln	145	150	155	160
Gly	Ile	Val	Ala	Thr	Ala	Gln	Phe	Glu	Ile	Tyr	Val	Lys	Trp	Ala	Pro	165	170	175	
Pro	Leu	Glu	Arg	Gly	Arg	Leu	Thr	Ser	Met	Ser	Thr	Ser	Gly	Phe	Leu	180	185	190	
Leu	Gly	Pro	Phe	Ile	Val	Leu	Leu	Val	Thr	Gly	Val	Ile	Cys	Glu	Ser				

195					200					205					
Leu	Gly	Trp	Pro	Met	Val	Phe	Tyr	Ile	Phe	Gly	Ala	Cys	Gly	Cys	Ala
210						215					220				
Val	Cys	Leu	Leu	Trp	Phe	Val	Leu	Phe	Tyr	Asp	Asp	Pro	Lys	Asp	His
225					230					235					240
Pro	Cys	Ile	Ser	Ile	Ser	Glu	Lys	Glu	Tyr	Ile	Thr	Ser	Ser	Leu	Val
				245					250					255	
Gln	Gln	Val	Ser	Ser	Ser	Arg	Gln	Ser	Leu	Pro	Ile	Lys	Ala	Ile	Leu
			260					265					270		
Lys	Ser	Leu	Pro	Val	Trp	Ala	Ile	Ser	Ile	Gly	Ser	Phe	Thr	Phe	Phe
		275					280					285			
Trp	Ser	His	Asn	Ile	Met	Thr	Leu	Tyr	Thr	Pro	Met	Phe	Ile	Asn	Ser
		290				295					300				
Met	Leu	His	Val	Asn	Ile	Lys	Glu	Asn	Gly	Phe	Leu	Ser	Ser	Leu	Pro
305					310					315					320
Tyr	Leu	Phe	Ala	Trp	Ile	Cys	Gly	Asn	Leu	Ala	Gly	Gln	Leu	Ser	Asp
				325					330					335	
Phe	Phe	Leu	Thr	Arg	Asn	Ile	Leu	Ser	Val	Ile	Ala	Val	Arg	Lys	Leu
			340					345					350		
Phe	Thr	Ala	Ala	Gly	Phe	Leu	Leu	Pro	Ala	Ile	Phe	Gly	Val	Cys	Leu
		355					360					365			
Pro	Tyr	Leu	Ser	Ser	Thr	Phe	Tyr	Ser	Ile	Val	Ile	Phe	Leu	Ile	Leu
		370				375					380				
Ala	Gly	Ala	Thr	Gly	Ser	Phe	Cys	Leu	Gly	Gly	Val	Phe	Ile	Asn	Gly
385					390					395					400
Leu	Asp	Ile	Ala	Pro	Arg	Tyr	Phe	Gly	Phe	Ile	Lys	Ala	Cys	Ser	Thr
				405					410					415	
Leu	Thr	Gly	Met	Ile	Gly	Gly	Leu	Ile	Ala	Ser	Thr	Leu	Thr	Gly	Leu
			420					425					430		
Ile	Leu	Lys	Gln	Asp	Pro	Glu	Ser	Ala	Trp	Phe	Lys	Thr	Phe	Ile	Leu
		435					440					445			
Met	Ala	Ala	Ile	Asn	Val	Thr	Gly	Leu	Ile	Phe	Tyr	Leu	Ile	Val	Ala
		450				455					460				
Thr	Ala	Glu	Ile	Gln	Asp	Trp	Ala	Lys	Glu	Lys	Gln	His	Thr	Arg	Leu
465					470					475					480

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Region

(B) LOCATION: 1..470

(D) OTHER INFORMATION: /note= "NPT3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Asp	Gly	Lys	Pro	Ala	Thr	Arg	Lys	Gly	Pro	Asp	Phe	Cys	Ser	Leu	1	5	10	15
Arg	Tyr	Gly	Leu	Ala	Leu	Ile	Met	His	Phe	Ser	Asn	Phe	Thr	Met	Ile	20	25	30	
Thr	Gln	Arg	Val	Ser	Leu	Ser	Ile	Ala	Ile	Ile	Ala	Met	Val	Asn	Thr	35	40	45	
Thr	Gln	Gln	Gln	Gly	Leu	Ser	Asn	Ala	Ser	Thr	Glu	Gly	Pro	Val	Ala	50	55	60	
Asp	Ala	Phe	Asn	Asn	Ser	Ser	Ile	Ser	Ile	Lys	Glu	Phe	Asp	Thr	Lys	65	70	75	80
Ala	Ser	Val	Tyr	Gln	Trp	Ser	Pro	Glu	Thr	Gln	Gly	Ile	Ile	Phe	Ser	85	90	95	
Ser	Ile	Asn	Tyr	Gly	Ile	Ile	Leu	Thr	Leu	Ile	Pro	Ser	Gly	Tyr	Leu	100	105	110	
Ala	Gly	Ile	Phe	Gly	Ala	Lys	Lys	Met	Leu	Gly	Ala	Gly	Leu	Leu	Ile	115	120	125	
Ser	Ser	Leu	Leu	Thr	Leu	Phe	Thr	Pro	Leu	Ala	Ala	Asp	Phe	Gly	Val	130	135	140	
Ile	Leu	Val	Ile	Met	Val	Arg	Thr	Val	Gln	Gly	Met	Ala	Gln	Gly	Met	145	150	155	160
Ala	Trp	Thr	Gly	Gln	Phe	Thr	Ile	Trp	Ala	Lys	Trp	Ala	Pro	Pro	Leu	165	170	175	
Glu	Arg	Ser	Lys	Leu	Thr	Thr	Ile	Ala	Gly	Ser	Gly	Ser	Ala	Phe	Gly	180	185	190	
Ser	Phe	Ile	Ile	Leu	Cys	Val	Gly	Gly	Leu	Ile	Ser	Gln	Ala	Leu	Ser	195	200	205	
Trp	Pro	Phe	Ile	Phe	Tyr	Ile	Phe	Gly	Ser	Thr	Gly	Cys	Val	Cys	Cys	210	215	220	
Leu	Leu	Trp	Phe	Thr	Val	Ile	Tyr	Asp	Asp	Pro	Met	His	His	Pro	Cys	225	230	235	240
Ile	Ser	Val	Arg	Glu	Lys	Glu	His	Ile	Leu	Ser	Ser	Leu	Ala	Gln	Gln	245	250	255	
Pro	Ser	Ser	Pro	Gly	Arg	Ala	Val	Pro	Ile	Lys	Ala	Met	Val	Thr	Cys	260	265	270	

Leu Pro Leu Trp Ala Ile Phe Leu Gly Phe Phe Ser His Phe Trp Leu  
 275 280 285  
 Cys Thr Ile Ile Leu Thr Tyr Leu Pro Thr Tyr Ile Ser Thr Leu Leu  
 290 295 300  
 His Val Asn Ile Arg Asp Ser Gly Val Leu Ser Ser Leu Pro Phe Ile  
 305 310 315 320  
 Ala Ala Ala Ser Cys Thr Ile Leu Gly Gly Gln Leu Ala Asp Phe Leu  
 325 330 335  
 Leu Ser Arg Asn Leu Leu Arg Leu Ile Thr Val Arg Lys Leu Phe Ser  
 340 345 350  
 Ser Leu Asp Met Gln Val Ser Ser Trp Glu Xaa Xaa Xaa Xaa Xaa Xaa  
 355 360 365  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Gln Gly  
 370 375 380  
 Asp Leu Gly Ser Ser Gln Glu Ser Xaa Ser Leu Pro Leu Pro Leu Asp  
 385 390 395 400  
 Ser Ser Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Arg Ile Leu  
 405 410 415  
 Ser Leu Val Gly Gly Met Ser Phe Ser Cys Leu Leu Xaa Xaa Xaa Xaa  
 420 425 430  
 Xaa Gln Ser Thr Cys Leu Ala Trp Ser Phe Thr Ser Arg Leu Asp Lys  
 435 440 445  
 Gln Asn Phe Lys Thr Gly Pro Lys Arg Gly Pro Leu Pro Ala Ser Glu  
 450 455 460  
 Asp Ile Lys Leu Gln Thr  
 465 470

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: /note= "NPT4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gln Val Asp Glu Thr Leu Ile Pro Arg Lys Gly Pro Ser Leu Cys  
 1 5 10 15  
 Ser Ala Arg Tyr Gly Ile Ala Leu Val Leu His Phe Cys Asn Phe Thr

20					25					30					
Thr	Ile	Ala	Gln	Asn	Val	Ile	Met	Asn	Ile	Thr	Met	Val	Ala	Met	Val
		35					40					45			
Asn	Ser	Thr	Ser	Pro	Gln	Ser	Gln	Leu	Asn	Asp	Ser	Ser	Glu	Xaa	Xaa
	50					55					60				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70					75					80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Leu	Pro	Val	Asp
				100				105					110		
Ser	Phe	Gly	Gly	Leu	Ser	Lys	Ala	Pro	Lys	Ser	Leu	Pro	Xaa	Xaa	Xaa
		115					120					125			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	130					135					140				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Lys
145					150					155					160
Ser	Ser	Ile	Leu	Gly	Gly	Gln	Phe	Ala	Ile	Trp	Glu	Lys	Trp	Gly	Pro
				165					170					175	
Pro	Gln	Glu	Arg	Ser	Arg	Leu	Cys	Ser	Ile	Ala	Leu	Ser	Gly	Met	Leu
			180					185					190		
Leu	Gly	Cys	Phe	Thr	Ala	Ile	Leu	Ile	Gly	Gly	Phe	Ile	Ser	Glu	Thr
		195					200					205			
Leu	Gly	Trp	Pro	Phe	Val	Phe	Tyr	Ile	Phe	Gly	Gly	Val	Gly	Cys	Val
	210					215					220				
Cys	Cys	Leu	Leu	Trp	Phe	Val	Val	Ile	Tyr	Asp	Asp	Pro	Phe	Ser	Tyr
225					230					235					240
Pro	Trp	Ile	Ser	Thr	Ser	Glu	Lys	Glu	Tyr	Ile	Ile	Ser	Ser	Leu	Lys
				245					250					255	
Gln	Gln	Val	Gly	Ser	Ser	Lys	Gln	Pro	Leu	Pro	Ile	Lys	Ala	Met	Leu
			260					265					270		
Arg	Ser	Leu	Pro	Ile	Trp	Ser	Ile	Cys	Leu	Gly	Cys	Phe	Ser	His	Gln
		275					280					285			
Trp	Leu	Val	Ser	Thr	Met	Val	Val	Tyr	Ile	Pro	Thr	Tyr	Ile	Ser	Ser
	290					295					300				
Val	Tyr	His	Val	Asn	Ile	Arg	Asp	Asn	Gly	Leu	Leu	Ser	Ala	Leu	Pro
	305				310					315					320
Phe	Ile	Val	Ala	Trp	Val	Ile	Gly	Met	Val	Gly	Gly	Tyr	Leu	Ala	Asp
				325					330					335	
Phe	Leu	Leu	Thr	Lys	Xaa	Lys	Phe	Arg	Leu	Ile	Thr	Val	Arg	Lys	Ile
			340					345					350		

Ala Thr Ile Leu Gly Ser Leu Pro Ser Ser Ala Leu Ile Val Ser Leu  
           355                          360                          365

Pro Tyr Leu Asn Ser Gly Tyr Ile Thr Ala Thr Ala Leu Leu Thr Leu  
       370                          375                          380

Ser Cys Gly Leu Ser Thr Leu Cys Gln Ser Gly Ile Tyr Ile Asn Val  
   385                          390                          395                          400

Leu Asp Ile Ala Pro Arg Tyr Ser Ser Phe Leu Met Gly Ala Ser Arg  
                           405                          410                          415

Gly Phe Ser Ser Ile Ala Pro Val Ile Val Pro Thr Val Ser Gly Phe  
                           420                          425                          430

Leu Leu Ser Gln Asp Pro Glu Phe Gly Trp Arg Asn Val Phe Phe Leu  
       435                          440                          445

Leu Phe Ala Val Asn Leu Leu Gly Leu Leu Phe Tyr Leu Ile Phe Gly  
       450                          455                          460

Glu Ala Asp Val Gln Glu Trp Ala Lys Glu Arg Lys Leu Thr Arg Leu  
   465                          470                          475                          480

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..2882
- (D) OTHER INFORMATION: /note= "cDNA 21"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGACCCACGC GTCCGAACAT GGCGACCTAG GAGAAAGGGA AGAACAATTT TTTCTCCTCT	60
TTTGGAAGG TTTGCGTCTA GTAGTGCCTG TGCCCTGGG CAGATTGGAG AGAAGAGGGA	120
CGACTGGAGA ATCGTCGAGA ACCAGCGGAG AAAAGAAAAA GCAACGTTTA ATTCTAGAAG	180
GCCTCCTGTC CCTGCCTGCT CTGGGTGCTC ATGGAATCAG CTGCTGCCCT GCACTTCTCC	240
CGGCCAGCCT CCCTCCTCCT CCTCCTCCTC AGCCTGTGTG CACTGGTCTC AGCCCAGTTT	300
ATTGTCGTGG GGGCCACTGA TCCCATCTTG GCCACGGTTG GAGAAAACAC TACGTTACGC	360
TGCCATCTGT CACCCGAGAA AAATGCTGAG GACATGGAGG TGCGGTGGTT CCGGTCTCAG	420
TTCTCCCCCG CAGTGTTTGT GTATAAAGGT GGCAGAGAGA GAACAGAGGA GCAGATGGAG	480
GAGTACCGAG GAAGAACCAC CTTTGTGAGC AAAGACATCA GCAGGGGCAG CGTGGCCCTG	540

GTCATACACA	ACATCACAGC	CCAGGAAAAC	GGCACCTACC	GCTGTTACTT	CCAAGAAGGC	600
AGGTCCTACG	ATGAGGCCAT	CCTGCACCTC	GTAGTGGCAG	GACTAGGCTC	TAAGCCCCCTC	660
ATTTCAATGA	GGGGCCATGA	AGACGGGGGC	ATCCGGCTGG	AGTGCATATC	TAGAGGGTGG	720
TACCCAAAGC	CCCTCACAGT	GTGGAGGGAC	CCCTACGGTG	GGGTTGCGCC	TGCCCTGAAA	780
GAGGTCTCCA	TGCCTGATGC	AGACGGCCTC	TTCATGGTCA	CCACGGCTGT	GATCATCAGA	840
GACAAGTCTG	TGAGGAACAT	GTCTGTCTCT	ATCAACAACA	CCCTGCTCGG	CCAGAAGAAA	900
GAAAGTGTCA	TTTTTATTCC	AGAATCCTTT	ATGCCCAGTG	TGTCTCCCTG	TGCAGTGGCC	960
CTGCCTATCA	TTGTGGTTAT	TCTGATGATA	CCCATTGCCG	TATGCATCTA	TTGGATCAAC	1020
AAACTCCAAA	AGGAAAAAAA	GATTCTGTCA	GGGGAAAAGG	AGTTTGAACG	GGAAACAAGA	1080
GAAATTGCTC	TAAAGGAACT	GGAGAAAGAA	CGTGTGCAAA	AAGAGGAAGA	ACTTCAAGTA	1140
AAAGAGAAAC	TTCAAGAAGA	ATTGCGATGG	AGAAGAACAT	TCTTACATGC	TGTTGATGTG	1200
GTCCTGGATC	CAGACACCGC	TCATCCCGAT	CTCTTCCTGT	CAGAGGACCG	GAGAAGTGTG	1260
AGAAGGTGCC	CCTTCAGGCA	CCTAGGGGAG	AGCGTGCTTG	ACAACCCAGA	GAGATTTCGAC	1320
AGTCAGCCTT	GTGTCCTAGG	CCGGGAGAGC	TTCGCTTCAG	GGAAACATTA	CTGGGAGGTG	1380
GAGGTGGAAG	ACGTGATTGA	GTGGACTGTG	GGGGTCTCTA	GAGACAGTGT	TGAGAGGAAA	1440
GGGGAGGTCC	TGCTGATTCC	TCAGAAATGGC	TTCTGGACCT	TGGAGATGCA	TAAAGGGCAA	1500
TACCGGGCCG	TGTCCTCCCC	TGATAGGATT	CTCCCTTTGA	AGGAGTCCCT	TTGCCGGGTG	1560
GGCGTCTTCC	TGGACTATGA	AGCTGGAGAT	GTCTCCTTCT	ACAACATGAG	GGACAGATCG	1620
CACATCTACA	CATGTCCCCG	TTCAGCCTTT	TCCGTGCCTG	TGAGGCCCTT	CTTCAGGTTG	1680
GGGTGTGAGG	ACAGCCCCAT	CTTCATCTGC	CCTGCACTCA	CAGGAGCCAA	TGGGGTCACG	1740
GTGCCTGAAG	AGGGCCTGAC	ACTTCACAGA	GTGGGGACCC	ACCAGAGCCT	ATAGAATCAA	1800
TTCCTTGGTC	TCACAGCCAT	GACAGACAAGC	CCTGGTCATC	TCAGCAGCCA	CCGCACAACA	1860
CCCCTGGTGG	AAGACACGCC	CTCCTCCCCT	CTGGTCACAC	AAGAGAACAT	CTTCCAGCTG	1920
CCTCTTTTAC	ACCCACTACA	GACCTCAGCC	CCAGTTTCTT	CCTCCTCACT	AGGCTGTGTT	1980
TTTAGTAGTT	CCTTTGCTTG	TAACTATGGG	ATGGGATCCA	GGCATAGGGA	ACTAGTTGTT	2040
ACACAGCTCC	CAGCCAAGAA	GAAAGTGTGA	GAAGTTGATG	GGCAGCAAAC	CTGCTGTTTA	2100
ACATCAGGGT	GACCACATTA	AGCCCAGTAT	TCCAGTTGGC	ACCAGAAGAT	ATGGACTTGG	2160
AATGAGGCCT	ACAGGGTTCA	CCAGGATGTA	AGAGGAGAGA	GGAATCCACA	GGACCACCAG	2220
AGAGGAGAGG	GAACCAGATA	TGCAGATCAG	AGATAGAGGA	AGTGGAACCA	GAGAGCTGGG	2280
AGGGACCAAG	GTTGTAAGGG	TGGCTAAGTC	CCACCATAAC	AGCTAAGGGG	ACCTGGGAGA	2340
TGATGGCTCA	TTTCCACCCA	GCCCCAGGAT	TTCCAGAGCG	CACATCCACA	GGCCTGGACC	2400

TGGGATGAAG ATGAATGAAG AACATGGATG CACGTGGATG TAGTTTGGCT CAGGTGTCCC	2460
TGCAGTTGGC AAGGAGTCAG TACTCAGTCC CTGAGTGTGG CTGAAATTTG AGGTCCTGGC	2520
TGAGCCAAGG AGTAATGGAC CAGATCTACC TCAGTATTCA AGTTCAGTGG GGACACCAAGT	2580
GGCTTCAAAC TTCCTGGTTT CATGATATCT TGAGACGCCT TACAAATGAT GGAGGATTCC	2640
AAAGAGTTTT TGTATTATTG GGTAAATATT TGTGGTATT TATGGCATT TATGATTGAAA	2700
CTAAGAAATG TTTTAATTTA TTACCTTTAC AACATTTATT TACATTACAT ACATACATT	2760
ACAACATTTA TTAATTTATA TTAATAAGC ATGAATAAGC CAATTATAGG TTAATATAAG	2820
TAGAATGTTT GTGAAAAATA AGTATGGTAT CCAAAGCAAA ATAAATTTTA TTGTGAAGTG	2880
TG	2882

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..2926
- (D) OTHER INFORMATION: /note= "cDNA 29"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGCGTCCGC TTCGGAATGA GAGACTCAAC CATAATAGAA AGAATGGAGA ACTATTAACC	60
ACCATTCTTC AGTGGGCTGT GATTTTCAGA GGGGAATACT AAGAAATGGT TTTCCATACT	120
GGAACCCAAA GGTAAGACA CTCAAGGACA GACATTTTGT GCAGAGCATA GATGAAAATG	180
GCAAGTTCCC TGGCTTTCCT TCTGCTCAAC TTTCATGTCT CCCTCTTCTT GGTCCAGCTG	240
CTCACTCCTT GCTCAGCTCA GTTTTCTGTG CTGGGACCCCT CTGGGCCCAT CCTGGCCATG	300
GTGGGTGAAG ACGCTGATCT GCCCTGTCAC CTGTTCCCGA CCATGAGTGC AGAGACCATG	360
GAGCTGAGGT GGGTGAGTTC CAGCCTAAGG CAGGTGGTGA ACGTGTATGC AGATGGAAAG	420
GAAGTGGAAG ACAGGCAGAG TGCACCATAT CGAGGGAGAA CTTCGATTCT GCGGGATGGC	480
ATCACTGCAG GGAAGGCTGC TCTCCGAATA CACAACGTCA CAGCCTCTGA CAGTGGAAG	540
TACTTGTGTT ATTTCCAAGA TGGTGAATTC TACGAAAAAG CCCTGGTGGA GCTGAAGGTT	600
GCAGCATTGG GTTCTGATCT TCACATTGAA GTGAAGGGTT ATGAGGATGG AGGGATCCAT	660
CTGGAGTGCA GGTCCACTGG CTGGTACCCC CAACCCCAAA TAAAGTGGAG CGACACCAAG	720
GGAGAGAACA TCCCGGCTGT GGAAGCACCT GTGGTTGCAG ATGGAGTGGG CCTGTATGCA	780

GTAGCAGCAT	CTGTGATCAT	GAGAGGCAGC	TCTGGTGGGG	GTGTATCCTG	CATCATCAGA	840
AATTCCCTCC	TCGGCCTGGA	AAAGACAGCC	AGCATATCCA	TCGCAGACCC	CTTCTTCAGG	900
AGCGCCCAGC	CCTGGATCGC	GGCCCTGGCA	GGGACCCTGC	CTATCTCGTT	GCTGCTTCTC	960
GCAGGAGCCA	GTTACTTCTT	GTGGAGACAA	CAGAAGGAAA	AAATTGCTCT	GTCCAGGGAG	1020
ACAGAAAGAG	AGCGAGAGAT	GAAAGAAATG	GGATACGCTG	CAACAGAGCA	AGAAATAAGC	1080
CTAAGAGAGA	AGCTCCAGGA	GGAACCTCAAG	TGGAGGAAAA	TCCAGTACAT	GGCTCGTGGA	1140
GAGAAGTCTT	TGGCCTATCA	TGAATGGAAA	ATGGCCCTCT	TCAAACCTGC	GGATGTGATT	1200
CTGGATCCAG	ACACGGCAAA	CGCCATCCTC	CTTGTTTCTG	AGGACCAGAG	GAGTGTGCAG	1260
CGTGCTGAAG	AGCCGCGGGA	TCTGCCAGAC	AACCCTGAGA	GATTTGAATG	GCGTTACTGT	1320
GTCCTTGGCT	GTGAAAACCT	CACATCAGGG	AGACATTACT	GGGAGGTGGA	AGTGGGGGAC	1380
AGAAAAGAGT	GGCATATTGG	GGTATGTAGT	AAGAACGTGG	AGAGGAAAAA	AGGTTGGGTC	1440
AAAATGACAC	CGGAGAACGG	ATACTGGACT	ATGGGCCTGA	CTGATGGGAA	TAAGTATCGG	1500
GCTCTCACTG	AGCCCAGAAC	CAACCTGAAA	CTTCTTGAGC	CTCCTAGGAA	AGTGGGGATC	1560
TTCCTGGACT	ATGAGACTGG	AGAGATCTCG	TTCTATAATG	CCACAGATGG	ATCTCATATC	1620
TACACCTTTC	CGCACGCCTC	TTTCTCTGAG	CTCTATATATC	CTGTTTTTCAG	AATTTTGACC	1680
TTGGAGCCCA	CTGCCCTGAC	CATTTGCCCA	ATACCAAAAG	AAGTAGAGAG	TTCCCCCGAT	1740
CCTGACCTAG	TGCCTGATCA	TTCCCTGGAG	ACACCACTGA	CCCCGGGCTT	AGCTAATGAA	1800
AGTGGGGAGC	CTCAGGCTGA	AGTAACATCT	CTGCTTCTCC	CTGCCCCACC	TGGAGCTGAG	1860
GTCTCCCCTT	CTGCAACAAC	CAATCAGAAC	CATAAGCTAC	AGGCACGCAC	TGAAGCACTT	1920
TACTGATATT	CATTCCATTA	TTCCATATGA	CAGTTGTTTT	GAGTTTCGTA	CCACCTTATT	1980
GTCCCCTTAT	ACAGATAAGG	AAACTGGGGT	GCAGAAAGGT	GAATTAACCT	TACAAAGTAG	2040
ACATGACAAG	TGAACAGCAG	AGCTGGGATC	TAAACAGCAA	TAACTAACAT	TAACAGAGAA	2100
TTTAAATGT	TCTTAGTGCT	GTGTTATAAG	CTTTGGTGGA	TGTCACCTCT	TTAATCCTCA	2160
CAACACCCTG	TCGGGTAGTC	ATATTTTGCA	AGTATGGAAG	CTGAGGCAGG	GCAACATGAA	2220
GTAACCTTACA	TAATTCATAC	AGTAATTTGT	GCAGTTGGGA	GATGTTCAGC	CTTAGTCCCT	2280
GGCTAATTGC	CTGTTCTTTT	CCAGCCTGAT	TTTTTTTCCC	ACAGGAAGAG	CCCACATGTA	2340
GCCCTGAGGT	TTCTTTCCCA	GGACAGCTGC	AGGGTAGAGA	TCATTTTAAG	TGCTTGTGGA	2400
GTTGACATCC	CTATTGACTC	TTTCCCAGCT	GATATCAGAG	ACTTAGACCC	AGCACTCCTT	2460
GGATTAGCTC	TGCAGAGTGT	CTTGGTTGAG	AGAATAACCT	CATAGTACCA	ACATGACATG	2520
TGACTTGGA	AGAGACTAGA	GGCCACACTT	GATAAATCAT	GGGGCACAGA	TATGTTCCCA	2580
CCCAACAAAT	GTGATAAGTG	ATTGTGCAGC	CAGAGCCAGC	CTTCCTTCAA	TCAAGGTTTC	2640

CAGGCAGAGC AAATACCCTA GAGATTCTCT GTGATATAGG AAATTTGGAT CAAGGAAGCT 2700  
 AAAAGAATTA CAGGGATGTT TTTAATCCCA CTATGGACTC AGTCTCCTGG AAATAGGTCT 2760  
 GTCCACTCCT GGTCATTGGT GGATGTTAAA CCCATATTCC TTTCAACTGC TGCCTGCTAG 2820  
 GGAAAACCTGC TCCTCATTAT CATCACTATT ATTGCTCACC ACTGTATCCC CTCTACTTGG 2880  
 CAAGTGGTTG TCAAGTTCTA GTTGTTCAT AAATGTGTTA ATAATG 2926

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..1645
- (D) OTHER INFORMATION: /note= "cDNA 23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATTTGCTTTC TCTTTTTCCT TTCTTCCGGA TGAGAGGCTA AGCCATAATA GAAAGAATGG 60  
 AGAATTATTG ATTGACCGTC TTTATTCTGT GGGCTCTGAT TCTCCAATGG GAATACCAAG 120  
 GGATGGTTTT CCATACTGGA ACCCAAAGGT AAAGACACTC AAGGACAGAC ATTTTGGCA 180  
 GAGCATAGAT GAAAATGGCA AGTTCCCTGG CTTTCTTCT GCTCAACTTT CATGTCTCCC 240  
 TCCTCTTGGT CCAGCTGCTC ACTCCTTGCT CAGCTCAGTT TTCTGTGCTT GGACCCTCTG 300  
 GGCCCATCCT GGCCATGGTG GGTGAAGACG CTGATCTGCC CTGTACCTG TTCCCGACCA 360  
 TGAGTGCAGA GACCATGGAG CTGAAGTGGG TAAGTTCCAG CCTAAGGCAG GTGGTGAACG 420  
 TGTATGCAGA TGGAAAGGAA GTGGAAGACA GGCAGAGTGC ACCGTATCGA GGGAGAACTT 480  
 CGATTCTGCG GGATGGCATC ACTGCAGGGA AGGCTGCTCT CCGAATACAC AACGTCACAG 540  
 CCTCTGACAG TGGAAAGTAC TTGTGTTATT TCCAAGATGG TGAATTCTAT GAAAAAGCCC 600  
 TGGTGGAGCT GAAGGTTGCA GCACTGGGTT CTAATCTTCA CGTCGAAGTG AAGGGTTATG 660  
 AGGATGGAGG GATCCATCTG GAGTGCAGGT CCACCGGCTG GTACCCCCAA CCCCAAATAC 720  
 AGTGGAGCAA CGCCAAGGGA GAGAACATCC CAGCTGTGGA AGCACCTGTG GTTGCAAGATG 780  
 GAGTGGGCCT ATATGAAGTA GCAGCATCTG TGATCATGAG AGGCGGCTCC GGGGAGGGTG 840  
 TATCCTGCAT CATCAGAAAT TCCCTCCTCG GCCTGGAAAA GACAGCCAGC ATTTCCATCG 900  
 CAGACCCCTT CTTCAGGAGC GCCCAGCCCT GGATCGCAGC CCTGGCAGGG ACCCTGCCTA 960  
 TCTTGCTGCT GCTTCTCGCC GGAGCCAGTT ACTTCTTGTG GAGACAACAG AAGGAAATAA 1020



CTGCTCTGTC CAGTGAGATA GAAAGTGAGC AAGAGATGAA AGAAATGGGA TATGCTGCAA	1080
CAGAGCGGGA AATAAGCCTA AGAGAGAGCC TCCAGGAGGA ACTCAAGAGG AAAAAATCCA	1140
GTACTTGACT CGTGGAGAGG AGTCTTCGTC CGATACCAAT AAGTCAGCCT GATGCTCTAA	1200
TGGAAAAATG GCCCTCTTCA AGCCTGGTGA GGAAATGCTT CAGATGAGGC TCCACCTTGT	1260
TAAATAAATT GGATGTATGG AAAAATAGAC TGCAGAAAAAG GGGAACTCAT TTAGCTCACG	1320
AGTGGTTCGAG TGAAGATTGA AAATTAACCT CTGAGGGCCA GCACAGCAGC TCATGCCTGT	1380
AATCCTAGCA CTTTGGAAGG CTGAGGAGGG CGGATCACAA GGTGAGGAGA TCAAGACCAT	1440
CCTGGCTAAC ACGGTGAAAC CCCGTCTCTA CTAAAAATAC AAAAAATAAA AAATTAGCCG	1500
GGCATGGTGA CGGGCACCTG TAGTCCCAGC TACTCGGGAG GCTGAGGCAG GAGAATGGCA	1560
TGAACCCGGA AGGCAGAGCT TGCAGTGAGC CGAGATCACG CCACTGCACT CCAGCCTGGG	1620
AGACAGAGCG AGACTCTGTC TCAAG	1645

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..3416
- (D) OTHER INFORMATION: /note= "cDNA 44"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGAAGCTTG CATGCCTGCA GGTCGACCCA CGCGTCCGCG GACGCGTGGG CGGACGCGTG	60
GGTTTTTCCT TTCTTCCAGA AGGAGATTTA ACCATAGTAG AAAGAATGGA GAACTATTAA	120
CTGCCTTCCT TCTGTGGGCT GTGATTTTCA GAGGGGAATG CTAAGAGGTG ATTTTCAATG	180
TTGGGACTCA AAGGTGAAGA CACTGAAGGA CAGAATTTTT GGCAGAGGAA AGATCTTCTT	240
CGGTCACCAT ACTTGAGTTA GCTCTAGGGA AGTGGAGGTT TCCATTTGGA ATTCTATAGC	300
TTCTTCCAGG TCATAGTGTC TGCCCCCACC CTTCCAGTAT CTCCTGATAT GCAGCATGAA	360
TGAAAATGGC AAGTTTCCTG GCCTTCCTTC TGCTCAACTT TCGTGTCTGC CTCCTTTTGC	420
TTCAGCTGCT CATGCCTCAC TCAGCTCAGT TTTCTGTGCT TGGACCCTCT GGGCCCATCC	480
TGGCCATGGT GGGTGAAGAC GCTGATCTGC CCTGTCACCT GTTCCCGACC ATGAGTGCAG	540
AGACCATGGA GCTGAAGTGG GTGAGTTCCA GCCTAAGGCA GGTGGTGAAC GTGTATGCAG	600
ATGGAAAGGA AGTGAAGAC AGGCAGAGTG CACCGTATCG AGGGAGAACT TCGATTCTGC	660

GGGATGGCAT	CACTGCAGGG	AAGGCTGCTC	TCCGAATACA	CAACGTCACA	GCCTCTGACA	720
GTGGAAAGTA	CTTGTGTTAT	TTCCAAGATG	GTGACTTCTA	TGAAAAAGCC	CTGGTGGAGC	780
TGAAGGTTGC	AGCACTGGGT	TCTGATCTTC	ACGTTGATGT	GAAGGGTTAC	AAGGATGGAG	840
GGATCCATCT	GGAGTGCAGG	TCCACTGGCT	GGTACCCCCA	ACCCCAAATA	CAGTGGAGCA	900
ACAACAAGGG	AGAGAACATC	CCGACTGTGG	AAGCACCTGT	GGTTGCAGAC	GGAGTGGGCC	960
TGTATGCAGT	AGCAGCATCT	GTGATCATGA	GAGGCAGCTC	TGGGGAGGGT	GTATCCTGTA	1020
CCATCAGAAG	TTCCCTCCTC	GGCCTGGAAA	AGACAGCCAG	CATTTCCATC	GCAGACCCCT	1080
TCTTCAGGAG	CGCCCAGAGG	TGGATCGCCG	CCCTGGCACG	GACCCTGCCT	GTCTTGCTGC	1140
TGCTTCTTGG	GGGAGCCGGT	TACTTCCTGT	GGCAACAGCA	GGAGGAAAAA	AAGACTCAGT	1200
TCAGAAAGAA	AAAGAGAGAG	CAAGAGTTGA	GAGAAATGGC	ATGGAGCACA	ATGAAGCAAG	1260
AACAAAGCAC	AAGAGTGAAG	CTCCTGGAGG	AACTCAGATG	GAGAAGTATC	CAGTATGCAT	1320
CTCGGGGAGA	GAGACATTCA	GCCTATAATG	AATGGAAAAA	GGCCCTCTTC	AAGCCTGCGG	1380
ATGTGATTCT	GGATCCAAAA	ACAGCAAACC	CCATCCTCCT	TGTTTCTGAG	GACCAGAGGA	1440
GTGTGCAGCG	TGCCAAGGAG	CCCCAGGATC	TGCCAGACAA	CCCTGAGAGA	TTTAATTGGC	1500
ATTATTGTGT	TCTCGGCTGT	GAGAGCTTCA	TATCAGGGAG	ACATTACTGG	GAGGTGGAGG	1560
TAGGGGACAG	GAAAGAGTGG	CATATAGGGG	TGTGCAGTAA	GAATGTGCAG	AGAAAAGGCT	1620
GGGTCAAAAT	GACACCTGAG	AATGGATTCT	GGA <sup>1</sup> ACTATGGG	GCTGACTGAT	GGGAATAAGT	1680
ATCGGACTCT	AAGTGAAGCC	AGAACCAACC	TGA <sup>1</sup> ACTTCC	TAAGCCCCCT	AAGAAAGTGG	1740
GGGTCTTCCT	GGACTATGAG	ACTGGAGATA	TCTCATTCTA	CAATGCTGTG	GATGGATCGC	1800
ATATTCATAC	TTTCCTGGAC	GTCTCCTTCT	CTGAGGCTCT	ATATCCTGTT	TTCAGAATTT	1860
TGACCTTGGA	GCCCACGGCC	CTGAGTATTT	GTCCAGCGTG	AAAAGAAGAA	GAGAGTTCCT	1920
CCAATTCTGA	CCGAGTGCTG	ATCATTCCTT	AGAGACACCA	GTAACCCCGG	GCTTAGCTAA	1980
CGAAAGTGGG	GAGCCTCAGG	CTGAAGTAAC	TTTTCTCTGC	TTCTCCCTGC	CCAGCTCAGA	2040
GCTGAGGGCC	TCCCCCTCCA	CAGCAACCAA	TCACAACCAT	AAAGCTACAA	GCACGCACTG	2100
AAGCACTTTA	CTGATACTCA	TTCAATTATT	CATATGACAG	TTGTTTGAGT	TTGGTACCAT	2160
CTTATTTTCC	CCTTATACAG	ATAAGGAAAC	TGGGGTGCAG	AAAAGTGAAT	TGACTACAAA	2220
GTAGACATGA	CTAGTTAACA	ACACAGCTGG	GATCTAAACA	GCAATAACTA	ACATTAATGG	2280
AGAACTTAAA	ATGCTCTGAG	TGCTGTGTTA	TGAGCTTTGG	TGGATGTCAC	TCCTTTAATC	2340
CTCGCAACAC	CCTGTCGGGT	AGTCTCATTT	AGCAAGTATG	GAAGTTGAGG	CAGGGCAACA	2400
TTAAGCAACT	TACATAACTC	ATGCAGTAAT	TTCTGCAGTT	GGGAGATGTT	CAGCTTCAGT	2460
CCCCGGCCCT	ATGGCCGTTT	TTTTCCACCC	TGTTTCTTCC	CCCATAGGAA	GAACCCACCT	2520

GTAGCCCTGA	GGTTCTTTTC	CCAGGATGGC	TCCAGGATAA	GGATCACTGT	AGGTGGTTGT	2580
GGAGTTGACA	CCCCTGTTGA	CTCCTTCCCA	GCTGATTGTC	AGAGCCCTAG	ACCCAGCACG	2640
CCTTGGA	TGCTTGCAGA	GTGTCTTGGT	TGAGAGAATA	ACCTCACCGT	ACCCACATGA	2700
CACGTGATTT	GGAAAGAGAC	TAGAGGCCAC	ACTTGATAAA	TCATGGGGAA	CAGATGTGTT	2760
CCACCCAACA	AATGTGATAA	GTGATCATGC	AGCCAGAGCC	AGCCTTCCTT	CAATCAAGGT	2820
TTCCAGGCAG	AGCAAATACC	CTAGAGATTT	TCTGTGATAT	AGGAAATTTG	GATGAAGGGA	2880
GCTAGAAGAA	ATACAGGGAT	TTTTTTTTTT	TTTAAAGATG	GAGTCTTACT	CTGTTGCTAG	2940
GCTGGAGTGC	AGTGGTGCGA	TCTCAGCTCC	CTGCAACCTC	CACCTCCTGG	GTTCAAACAA	3000
TTCTCCTGCC	TCAGCCTCCC	GAGTACTGGG	AATATAGGTG	CACGCCACCA	CACCCAACAA	3060
ATTTTTGTAC	TTTTAGTACA	GATGAGGGTT	CACTATGTTG	GCCAGGATGG	TCTCGATCTC	3120
TTGACCTCAT	GATCCACCCA	CCTCGGTCTC	CCAAAGTGCT	GGGATTACAG	GCTTGAGCCA	3180
CCGGGTGACC	GGCTTACAGG	GATATTTTTA	ATCCCGTTAT	GGACTCTGTC	TCCAGGAGAG	3240
GGGTCTATCC	ACCCCTGCTC	ATTGGTGGAT	GTAAACCAA	TATTCCTTTC	AACTGCTGCC	3300
TGCTAGGGAA	AACTACTCC	TCATTATCAT	CATTATTATT	GCTCTCCACT	GTATCCCCTC	3360
TACCTGGCAT	GTGCTTGTC	AGTTCTAGTT	GTTCAATAAA	TTTGTTAATA	ATGCTG	3416

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..3502
- (D) OTHER INFORMATION: /note= "cDNA 32"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGAGAACAGG	TCCCAGATAC	CGAGTCCGCA	ACCCCAAACA	TCGCGATTAA	TAGGAGGCCT	60
CTGGTCTCTG	CCTGCCCTGG	GTGCTCATGG	AACCAGCTGC	TGCTCTGCAC	TTCTCCCTGC	120
CAGCCTCCCT	CCTCCTCCTC	CTGCTCCTCC	TCCTTCTCAG	CCTGTGTGCA	CTGGTCTCAG	180
CCCAGTTTAC	TGTCGTGGGG	CCAGCTAATC	CCATCCTGGC	CATGGTGGGA	GAAAACACTA	240
CATTACGCTG	CCATCTGTCA	CCCAGAAAAA	ATGCTGAGGA	CATGGAGGTG	CGGTGGTTCC	300
GGTCTCAGTT	CTCCCCCGCA	GTGTTTGTGT	ATAAGGGTGG	GAGAGAGAGA	ACAGAGGAGC	360
AGATGGAGGA	GTACCGGGGA	AGAATCACCT	TTGTGAGCAA	AGACATCAAC	AGGGGCAGCG	420

TGGCCCTGGT	CATACATAAC	GTCACAGCCC	AGGAGAATGG	GATCTACCGC	TGTTACTTCC	480
AAGAAGGCAG	GTCCTACGAT	GAGGCCATCC	TACGCCTCGT	GGTGGCAGGC	CTTGGGTCTA	540
AGCCCCTCAT	TGAAATCAAG	GCCCAAGAGG	ATGGGAGCAT	CTGGCTGGAG	TGCATATCTG	600
GAGGGTGGTA	CCCAGAGCCC	CTCACAGTGT	GGAGGGACCC	CTACGGTGAG	GTTGTGCCCCG	660
CCCTGAAGGA	GGTTTCCATC	GCTGATGCTG	ACGGCCTCTT	CATGGTCACC	ACAGCTGTGA	720
TCATCAGAGA	CAAGTATGTG	AGGAATGTGT	CCTGCTCTGT	CAACAACACC	CTGCTCGGCC	780
AGGAGAAGGA	AACTGTCATT	TTTATTCCAG	AATCCTTTAT	GCCCAGCGCA	TCTCCCTGGA	840
TGGTGGCCCT	AGCTGTCATC	CTGACCGCAT	CTCCCTGGAT	GGTGTCCATG	ACTGTCATCC	900
TGGCTGTTTT	CATCATCTTC	ATGGCTGTCA	GCATCTGTTG	CATCAAGAAA	CTTCAAAGGG	960
AAAAAAGAT	TCTGTCAGGG	GAAAAGAAAG	TTGAACAAGA	GGAAAAAGAA	ATTGCACAGC	1020
AACTTCAAGA	AGAATTGCGA	TGGAGAAGAA	CATTCTTACA	TGCTGCTGAT	GTGGTCCTGG	1080
ATCCAGACAC	CGCTCATCCC	GAGCTCTTCC	TGTCAGAGGA	CCGGAGAAGT	GTGAGGCGGG	1140
GCCCCTACAG	GCAGAGAGTG	CCTGACAACC	CAGAGAGATT	CGACAGTCAG	CCTTGTGTCC	1200
TGGGATGGGA	GAGCTTCGCC	TCAGGGAAAC	ATTACTGGGA	GGTGGAGGTG	GAAAACGTGA	1260
TGGTGTGGAC	TGTGGGGGTC	TGCAGACACA	GTGTTGAGAG	GAAAGGGGAG	GTCCTGCTGA	1320
TTCCTCAGAA	TGGCTTCTGG	ACCCTGGAGA	TGTTTGGAAA	CCAATACCGG	GCCCTGTCTT	1380
CCCCTGAGAG	GATTCTCCCT	TTGAAGGAGT	CCCTTTGCCG	GGTGGGCGTC	TTCCTGGACT	1440
ATGAAGCTGG	AGATGTCTCC	TTCTACAACA	TGAGGGACAG	ATCACACATC	TACACATGTC	1500
CCCGTTCAGC	CTTTACTGTG	CCTGTGAGGC	CCTTCTTCAG	GTTAGGGTCT	GATGACAGCC	1560
CCATCTTCAT	CTGCCCTGCA	CTCACAGGAG	CCAGTGGGGT	CATGGTGCCT	GAAGAGGGCC	1620
TGAAACTTCA	CAGAGTGGGG	ACCCACCAGA	GCCTATAGAA	TCAATTCCTT	GGACTCACAG	1680
CCATGCAGAT	AAGCCCTGGC	CATCTCAGCA	GCCACCGCAC	AACCCCCCTA	ATGAAAGACA	1740
CGCCCTCCTC	CCCTCTGGTC	ACGTAAGAGA	ACATCTTCCA	GCTGCCTTTT	TCACACCCAC	1800
TCCAGCCCTC	TGCCCCAGTT	TTCTCCTCCT	CACTAGTCTG	TGGCTTTAGT	AGTTCCTTTG	1860
CTTGTAATTA	TGGGATGGGA	TCCAGGCATA	GGGAACTAGT	TGTTTCATAG	CTCCCAGTCA	1920
AAAAGAAAGT	GAGAGAAGCT	GTTGGGCAGT	GAACCTACTG	TTTAAAATCA	GGATAACCAC	1980
ATTAAGCCCA	ATATGCCAGT	TGGCACCAGA	TGCTGTGGAC	TTGGAATGAG	GCCAACAGGG	2040
TTCACCAGGA	TGAGAGAGGA	GAGAGGAATC	CACAGGACCA	CCAGAAGGGA	GAGGGAACCA	2100
GATATGCAGA	TCAGAGATAG	AGGAAGTGGA	ACCAGAGAGC	TGGGAGGGAC	CAAGGTTGTA	2160
AGGATGGCTA	AGTCCCACCA	TAAGAGCTAA	AGGGTCCTGG	GAGATGATGG	CTCATTTCCA	2220
CCCAACCCCA	GGATTTCCAC	AGCACACACC	CACAGGCCTG	GACCTGGGAT	GAAGATGAAT	2280

GAAGAACATG GACTCATGTG GATGTGGTTT GGCTCAGATG TCCCTGCAAT AAACAAGGGG	2340
TCAGTACTTA GTCCCTGAGT GTGGTTGAGG TTTGAGGTCC TGGTCGAGCA GGGCAGTACT	2400
GGACCAGGTC TACGTCAGCA TTCAGGTTCA ATGGGGACAC CAGTGGCTTC AACTTCCTG	2460
ATCTAATTAT GTTTTTAGAC ACTTAGAAGT TATTGAGGAC TTAAAGAGC TTTTGTATTAT	2520
TTGGGTAAAT ATTTATGACA TTTGACATTG AAACAAAAAT TAAAAATGTT ATCTTTTAAT	2580
TTATGTTAAA ATAGCATTAA TAAATCAGTT ATAGGTTAAT GTAGATAGGA TGTTTTGTGA	2640
AAAAGCAATC TATTGTGTCC AAATAAAAAA AACAAAAAGT GTGACACTGG TTAACTTTTT	2700
CCAGATCTCA TGTCTGGCTT AATAAGAGAT ATTTGTATTA TCATATCTGC CTTTGTATTA	2760
AACCTATTGG TATATCATAG GTCATGTTAG CTCAAAAAAA CTTTACTGCA CACTACTGAG	2820
AGAATGAGAT GAAAAACGAT TAATGTTTCA TTATTATTAT TGTGAAAAATA TTATTAACAC	2880
TGGGGACTCC TTAAGAGTAC ATCAGAGTTC TCTCTAGGAA TCCCAAAACC ACATTTTGAA	2940
ACTAGAATAG TGGATCCTGG AAGTTAATCC ATGTGCTGGT TAATTTTAGA TGTCAACCTG	3000
GTGTTTCCAG AAGAGATTGG CAAGTGAGTC AGTGGGAAAT TCTCTCCTTC TGTTGGCTGG	3060
GTGCCCAATA CAACAAAAAG GCAGAGGAAA GGCAAATTCT TCTCTCCTCT GGAGCTGAGA	3120
CACTCTTCTT CTTCTGCCCT TGGACATCAG AACTCCTGGC TCTCCGGCCT TTGAACTTCA	3180
GGACTTGTAC CAGGAGGCCC TGGGTTCTCA GGCCTTTGGC TTTGGACTGA GAGTTACACA	3240
ATCAGCTTCC CTGGTTCTGA GGCTTTCAGA CTTAAACTGA GCCATGCTAC CAGCATCCCA	3300
GGGTCTCCAG CCTACAGATG AGCTGTTGTG CGATTTCTTA GCCTCCATAA TCACATGAGC	3360
CAATCTCCTT AATAAATGCC TGCTCATAGA TCTGTATCTA CATCTATATC TGTATGTGCA	3420
TCTATATCTA TGCCTATATC TATATCTATA TCATATTGAT TTTGTCTCTC TGGAGAACCC	3480
TGACTAATAA AATGAGGCAT CT	3502

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..2854
- (D) OTHER INFORMATION: /note= "cDNA 27"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACCCACGCG TCCGAAAAGC TATGGCCTCA ACCACCAGCA CCAAGAAGAT GATGGAGGAA	60
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GCCACCTGCT	CCATCTGCCT	GAGCCTGATG	ACGAACCCAG	TAAGCATCAA	CTGTGGACAC	120
AGCTACTGCC	ACTTGTGTAT	AACAGACTTC	TTTAAAAACC	CAAGCCAAAA	GCAACTGAGG	180
CAGGAGACAT	TCTGCTGTCC	CCAGTGTCGG	GCTCCATTTC	ATATGGATAG	CCTCCGACCC	240
AACAAGCAGC	TGGGAAGCCT	CATTGAAGCC	CTCAAAGAGA	CGGATCAAGA	AATGTCATGT	300
GAGGAACACG	GAGAGCAGTT	CCACCTGTTC	TGCGAAGACG	AGGGGCAGCT	CATCTGCTGG	360
CGCTGTGAGC	GGGCACCACA	GCACAAAGGG	CACACCACAG	CTCTTGTTGA	AGACGTATGC	420
CAGGGCTACA	AGGAAAAGCT	CCAGAAAGCT	GTGACAAAAC	TGAAGCAACT	TGAAGACAGA	480
TGTACGGAGC	AGAAGCTGTC	CACAGCAATG	CGAATAACTA	AATGGAAAGA	GAAGGTACAG	540
ATTCAGAGAC	AAAAAATCCG	GTCTGACTTT	AAGAATCTCC	AGTGTTTCCT	ACATGAGGAA	600
GAGAAGTCTT	ATCTCTGGAG	GCTGGAGAAA	GAAGAACAAC	AGACTCTGAG	TAGACTGAGG	660
GACTATGAGG	CTGGTCTGGG	GCTGAAGAGC	AATGAACTCA	AGAGCCACAT	CCTGGAAGTG	720
GAGGAAAAAT	GTCAGGGCTC	AGCCCAGAAA	TTGCTGCAGA	ATGTGAATGA	CACTTTGAGC	780
AGGAGTTGGG	CTGTGAAGCT	GGAAACATCA	GAGGCTGTCT	CCTTGGAAGT	TCATACTATG	840
TGCAATGTTT	CCAAGCTTTA	CTTCGATGTG	AAGAAAATGT	TAAGGAGTCA	TCAAGTTAGT	900
GTGACTCTGG	ATCCAGATAC	AGCTCATCAC	GAACATAATC	TCTCTGAGGA	TCGGAGACAA	960
GTGACTCGTG	GATACACCCA	GGAGAATCAG	GACACATCTT	CCAGGAGATT	TACTGCCTTC	1020
CCCTGTGTCT	TGGGTTGTGA	AGGCTTCACC	TCAGGAAGAC	GTTACTTTGA	AGTGGATGTT	1080
GGCGAAGGAA	CCGGATGGGA	TTTAGGAGTT	TGTATGGAAA	ATGTGCAGAG	GGGCACTGGC	1140
ATGAAGCAAG	AGCCTCAGTC	TGGATTCTGG	ACCCTCAGGC	TGTGCAAAAA	GAAAGGCTAT	1200
GTAGCACTTA	CTTCTCCCCC	AACTTCCCTT	CATCTGCATG	AGCAGCCCCC	GCTTGTGGGA	1260
ATTTTTCTGG	ACTATGAGGC	CGGAGTTGTA	TCCTTTTATA	ACGGGAATAC	TGGCTGCCAC	1320
ATCTTTACTT	TCCCGAAGGC	TTCCTTCTCT	GATACTCTCC	GGCCCTATTT	CCAGGTTTAT	1380
CAATATTCTC	CTTTGTTTCT	GCCTCCCCCA	GGTGACTAAG	GAAAAGAGCA	GAAGCTCCTT	1440
GGTTTAACCA	GCACAGAGAA	AATAATATAA	ATCCCATAAG	GGCAGACGTT	TGGTCTGTTT	1500
TCTTCGCTGT	CATTTCCCTA	GTAGTTAGAC	TAGTGCTGAG	ATTTTAGTGG	ATATATAATT	1560
GATTTATGTT	GAATATATGG	ACTTAGCAAC	TAAAAATACC	ACAGATGGTT	AACCTGGACT	1620
GGGGCAAAGC	AAGATAATAG	TGATGATCGT	ATGTTGCTGT	CTCCATCCGT	CTTTAATGGG	1680
TCAGGGCTTT	GATTTCCAAG	GGTCTTCAGG	TGATGAGTAG	GGGTACCCAC	AAGTCAGAAG	1740
GTCTGCGTTC	TCCTAGTTTG	TTTGCTGCCA	TTTGAACCTA	TGTAGGGAAT	GAAAGAAAGC	1800
TGCAATTATC	CGCCAACTGC	ATTTAAAACA	AAACAAAACA	GAAAAATCAA	AATAACATTG	1860
ACTCTTCCAA	CCACTGACAT	GTTGTTTAAAT	AATCTAAGCG	GCAGTCCTGG	AGGCTACCAG	1920

ACTTACTGAG TTCTACCTGA GAAACAGCCA AGCAAAGTGT GAGAGAAGGG TTAAGACTGG	1980
CTTACAATGA GATGCTTCAA ATGAAAAGGG AATTATGAGT AAAATTGAAC TTTGATGGGG	2040
GATTCAGTTC TGGAAAAGAA TTTGGTATTT TCCAGTCTGC TAGGACCAAT TACCTTGAAA	2100
TATTTTAAAA TCTCAGTAAA TAGTTATTGC TGAAATGGCT GTTGGCAGTT CTTATTATGA	2160
TTCAGAGAAG AGCAAATAGA CCTTAACCTC ATTTTGAAAA AGACCAAATT ACCATACCCG	2220
AGTGAGTAAT GACAGGACTA CAACTAAAAC ATAAACAACA TTAATGATGA CCATAAAAAG	2280
TCACAAAATT GCTAAATGTT ATAATTTAGA GTTGACATAA AAATTGATGG CCAGGCATGG	2340
TGGCTCACGC CTGTAATCCC AGAACTATGT GAGGCTGAGG CAGGTGGATC ACTTGAGGTC	2400
AGGAGTTCAA CACCAGCCTG GCCAACATGG TGAAACCCTG TCTCTACTAA AAATACAAAA	2460
ATTAGCCGGG CATGGTGGTA GGGGCCTGTA ACCCAGCTAC TCGTGAGGCC AAGGCAGGAG	2520
AATTGCTTGA GCCTGCAGCA GCTGCAGTAA GCCAAGATCA TGCTGTGCCT CAAGGAAAAA	2580
AAAAATTAAT GTTTACTGAT ATTTGTTGAA GTCCTACAAC ATCACCTCTG AGAATAGGAG	2640
AAATGAAGCA ACAGTTGTGT CTAGATGTCA GAGGCATGGC TGGGCCTCCA TCTCTGCCTA	2700
AGGGAGATAT AAAAGAGTTC AAATATTGC CCATGTTCCC CAGGGTCAGA AGTTCTAATT	2760
ATGATGATAG AGGCTGGGTT GTAAGTAGTA AGTGAAGGGT AGCAGAATAT GCCATCTTTG	2820
GCATAAGAAG TATTTTGAGT TGAAGACAAT TGAG	2854

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..2266
- (D) OTHER INFORMATION: /note= "cDNA 22B"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGACAGAAAA CTCCCTCCTT TTCCAAGTTA GCCTTATAGT CTAGGGCTTA AAATACTGGT	60
TTAATGGTGA AGGTAAGTGC TTTTCTTCTT TTTGGGTAGA AGGATTATTA CTAACCTACC	120
AAAGGTCCAT TAAGGGGAGG GAACAGTTTT AGGAGAAGTC AGAGAAAAGA CATTAAACAGC	180
AACATAAGGA TCTCCATCTG GTAATATTGC CTAATTCCAA AATGAAGAGA CTCTCTGAAA	240
AAGATAACTG ATTCAATGAA GACCCTAGGG CAAGGCTTGA GAAGCCACTG GTACCAATGG	300
CACTGTGGA CAATGGTCAT TTCTCCAAGG ACGCTATAAA AGACTGTCGT AGTAAAAGAG	360

ATTGAGGGCA	CAGGGAAACT	CCACCACAAA	GCGTGGTACC	ATTTCCCACA	GAAGCTAAAT	420
GGACGGGAAG	CCTGCCACCA	GGAAAGGTCC	AGATTCTGT	TCATTACGCT	ATGGGCTGGC	480
TCTTATCATG	CACTTCTCAA	ACTTCACCAT	GATAACGCAG	CGTGTGAGTC	TGAGCATTGC	540
GATCATCGCC	ATGGTGAACA	CCACTCAGCA	GCAAGGTCTA	TCTAATGCCT	CCACTGAGGG	600
GCCTGTTGCA	GATGCCTTCA	ATAACTCCAG	CATATCCATC	AAGGAATTTG	ATACAAAGGC	660
CTCTGTGTAT	CAATGGAGCC	CAGAAACTCA	GGGTATCATC	TTTAGCTCCA	TCAACTATGG	720
GATAATACTG	ACTCTGATCC	CAAGTGGATA	TTTAGCAGGG	ATATTTGGAG	CAAAAAAAT	780
GCTTGGTGCT	GGTTTGCTGA	TCTCTTCCCT	TCTCACCTC	TTTACACCAC	TGGCTGCTGA	840
CTTCGGAGTG	ATTTTGGTCA	TCATGGTTTC	GACAGTCCAG	GGCATGGCCC	AGGGAATGGC	900
ATGGACAGGT	CAGTTTACTA	TTTGGGCAAA	GTGGGCTCCT	CCACTTGAAC	GAAGCAAGCT	960
CACCACCATT	GCAGGATCAG	GGTCAGCATT	TGGATCCTTC	ATCATCCTCT	GTGTGGGGGG	1020
ACTAATCTCA	CAGGCCTTGA	GCTGGCCTTT	TATCTTCTAC	ATCTTTGGTA	GCACTGGCTG	1080
TGTCTGCTGT	CTCCTATGGT	TCACAGTGAT	TTATGATGAC	CCCATGCATC	ACCCGTGCAT	1140
AAGTGTTAGG	GAAAAGGAGC	ACATCCTGTC	CTCACTGGCT	CAACAGCCCA	GTTCTCCTGG	1200
ACGAGCTGTC	CCCATAAAGG	CGATGGTCAC	ATGCCCTACCA	CTTTGGGCCA	TTTTCTCTGG	1260
TTTTTTCAGC	CATTTCTGGT	TATGCACCAT	CATCCTAACA	TACCTACCAA	CGTATATCAG	1320
TACTCTGCTC	CATGTTAACA	TCAGAGATAG	TGGAGTTCTG	TCCTCCCTGC	CTTTTATTGC	1380
TGCTGCAAGC	TGTACAATTT	TAGGAGGTCA	GCTGGCAGAT	TTCTTTTGT	CCAGGAATCT	1440
TCTCAGATTG	ATCACTGTGC	GAAAGCTCTT	TTCATCTCTT	GATATGCAAG	TTTCTCATG	1500
GGAATCTCAA	GGGGATTTGG	GCTCATCGCA	GGAATCATCT	CTTCCACTGC	CACTGGATTTC	1560
CTCATCAGTC	AGGATTTTGA	GTCTGGTTGG	AGGAATGTCT	TTTTCTGTGC	TGCTGCAGTC	1620
AACATGTTTG	GCCTGGTCTT	TTACCTCACG	TTTGGACAAG	CAGAACTTCA	AGACTGGGCC	1680
AAAGAGAGGA	CCCTTACCCG	CCTCTGAGGA	CATAAAGTTA	CAAACTTAAA	TGTGGTACTG	1740
AGCATGAACT	TTTTAAACAT	TTTTTACTTC	TCTCCATATT	CCTGACCATA	GACTCAGCAG	1800
TTCTTAACTC	TGGCTGTGTG	TTAGTCTTCC	CTGGGGAGCC	TTTATAAGAC	ACTGATACTT	1860
GGGACCCACT	CCAGAGATTG	TGAATGAATT	GGTCTGGGGT	GGAACCCAGA	TACTACTAAT	1920
TTTTAGATAC	TCCTTAGAGG	TTTCTAGCAT	GCGCCCGGGG	TTGACAACAG	CTGGACAAAC	1980
TTGAAAAGTC	AATTCATGTG	GCCTTTGAAT	TTTCTCATT	GGAAAGTACT	AAATAAATAA	2040
AAATTCATGT	GAAAATGATC	ACTGATAAAT	ATCTTCATGG	TGGGGCAGGT	TATTGGATGC	2100
AGAGAAGATC	TGCTCGGAAT	TGTAGCCATA	TGTTACAGAT	CTCAGCACCG	ATCAGAACTG	2160
TAAAGCTATA	ATCCCAGAA	TTAAAGTTTT	TATTATTTTT	TATACATTGT	AAAACATAGA	2220



CGTTTATTTA TGTGATTAAA TTCTATTAAA ATTTACATGC TAAAAT

2266

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..1780
- (D) OTHER INFORMATION: /note= "cDNA 22E"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACGCGTCCGC CCACGCGTCC GCCACGCGT CCGGTCGGGG CCAGAGCGCA GGTGTACCTG	60
GCGGCCGTGC TGGAGCACCT GACCGCCGAG ATCCTGGAGC TGGCTGGCAA CCCGGCCCCG	120
GACAAGAAGA CCCGCATCAT CCTGCGCCAC CTGTAGCTGG CCATTGCAA CGGCGAGGAG	180
CTTAACAAGC TGCTGGGCGA AGTCACCATC GCGCAGGGCG GTGTCCTGCC CAACATTCA	240
GGCGTGCTTC TGCCCCAGAA GACCAAGAGC CACCAACAAG OCAAGGGTGA AAACCATTCA	300
CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCCACAG CAAGGGAGAG	360
CAAGAACGCA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT	420
ATGTTCTGCT CGCTATGGAA TAGCCCTCGT CTTACATTTC TGCAATTTC CAACGATAGC	480
ACAAAATGTC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACAA GCCCTCAATC	540
CCAGCTCAAT GATTCTCTG AGGTGCTGCC TGTGACTCA TTTGGTGGCC TAAGTAAAGC	600
CCCAAAGAGT CTTCTGCAA AGTCCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAAA	660
GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTTACT	720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCATTAGT GAAACCCTTG GGTGGCCCTT	780
TGTCTTCTAT ATCTTTGGAG GTGTTGGCTG TGTCTGCTGC CTTCTCTGGT TTGTTGTGAT	840
TTATGATGAC CCCTTTTCCT ATCCATGGAT AAGCACCTCA GAAAAAGAAT ACATCATATC	900
CTCCTTGAAA CAACAGGTCG GGTCTTCTAA GCAGCCTCTT CCCATCAAAG CTATGCTCAG	960
ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGGT TAGTTAGCAC	1020
AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA	1080
TGGACTTCTA TCTGCCCTTC CTTTTATTGT TGCCTGGGTC ATAGGCATGG TGGGAGGCTA	1140
TCTGGCAGAT TTCCTTCTAA CAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTGCCAC	1200
AATTTTAGGA AGTCTCCCCT CTTCAGCACT CATTGTGTCT CTGCCTTACC TCAATTCCGG	1260

CTATATCACA	GCAACTGCCT	TGCTGACGCT	CTCTTGCGGA	TTAAGCACAT	TGTGTCAGTC	1320
AGGGATTTAT	ATCAATGTCT	TAGATATTGC	TCCAAGGTAT	TCCAGTTTTC	TCATGGGAGC	1380
ATCAAGAGGA	TTTTCGAGCA	TAGCACCTGT	CATTGTACCC	ACTGTCAGCG	GATTTCTTCT	1440
TAGTCAGGAC	CCTGAGTTTG	GGTGGAGGAA	TGTCTTCTTC	TTGCTGTTTG	CCGTAAACCT	1500
GTTAGGACTA	CTCTTCTACC	TCATATTTGG	AGAAGCAGAT	GTCCAAGAAT	GGGCTAAAGA	1560
GAGAAACTC	ACTCGTTTAT	GAAGTTATCC	CACCTTGGAT	GGAAAAGTCA	TTAGGCACCG	1620
TATTGCATAA	AATAGAAGGC	TTCCGTGATG	AAAATACCAG	TGAAAAGATT	TTTTTTTCCT	1680
GTGGCTCTTT	TCAATTATGA	GATCAGTTCA	TTATTTTATT	CAGACTTTTT	TTTGAGAGAA	1740
ATGTAAGATG	AATAAAAATT	CAAATAAAAT	GATAACTAAG			1780

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..246240
- (D) OTHER INFORMATION: /note= "HLA-H.CONTIG"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGTAAGTA	TTCTATTTTA	TTTATATGTG	TTTGTGTTTC	TGAGTATGTC	CTGAGTTGCA	60
CGATAATACT	ATATTTCTTA	TTGGGTAACA	TTGTCAGAAA	AGTTTCTAAA	AACTTTCTCT	120
GCTGCACTTA	TTTTATACAT	TTTATTTATG	TTAATAATCT	CACATTTAAC	ACACTTATGA	180
TTTATTCTCA	ACAGAAAAAG	GTGGTATTTT	TTTCATTTAG	TCTTTTAAAA	AGCTCACATT	240
ATCAAATGAT	TGCTCAATCA	TTTAATCTCT	TTGCTTCTCT	TATATGCATT	GATTTAATAA	300
ATATGTATAC	TAGTTTCTCC	ATCGATTCTT	TAGATTTGAA	ACTTATTTTC	CTTTTATTCT	360
TACAAAAGTG	ACTTGTCTAT	AGGCCCACTT	CTACTTCCTT	TATTCTATCA	TCTTCCTCAA	420
CTTATTCTGT	GGTCAAAGAA	TGGAGAAATA	ATATTAATAA	TATGTTTTTC	TCATCAATGA	480
CTTCCACCTG	TTCTCTGAGA	AATTCAGCTT	CAAGAACTTT	AGTTTGATAT	GA CTGCAAAG	540
ATAATACACA	GTCTAAATCA	TAAAAATGTC	TCAAAGGTTT	TTTTTTTATT	TGTTTCTTTG	600
AAATATCCAT	GAACAGGCAT	GTTTCTCCCC	CTGTAGTGCA	ATTTGTGTGA	AATTCTGGCA	660
TGCACTTAAG	AGGATGTCCT	AAAATACCAA	TATTTAATTG	ATTCTAAGTC	ATGTATTGTA	720
TCACATTTTT	GCCCATGGAT	TGTTGAAATC	CATGGACAAA	ACTGATAGCA	TTTTAGAAGT	780

TCCTTTGTCT	AGTGGCAGTC	TTGATATATT	CACACTATCT	ATTGACAAAA	AATCTAAAGC	840
ACCAGGCTCA	AAGCTTGTAG	AGTAGGTGTC	AGTGATTGG	AGGACATCTC	TAGGGCAATA	900
GTAGAGGCAT	TTTTAACCCC	TAACAACATA	ATGATCATCA	GAAGTGAGTG	ATATCCTCAC	960
TCATGACCCC	AACTGCTCTA	ATTTCTATTG	TTTTCTTGCA	GAAATGAGAG	CAGGTGGGGT	1020
CATGGGTGAG	GAATGAGGTG	TTGAAAGTGA	ATGGGGTGTT	GAAAGCAAGG	TGTTTAGCAG	1080
TGTTCTGAAA	GCATACATTT	AAGTAGGCTA	TCCGGGCACT	GTCAATAGCT	AAGTGTCAG	1140
CTAAGTACTC	TATTTTATTC	TAAGAACTAT	TTTGTAGAAAT	GCTGAATCAA	CAAATCTCAG	1200
ATGGCACAGA	GGTTGTCATT	TTTGAATAAT	ATGAATATCA	GTAATTTTAG	TTGGAAAAGA	1260
AGATTTTCAA	AGAGCCATCT	AAGTTTCCAA	AATAAGTGTT	GCAGTCATAT	TAATATTAT	1320
ATTTTCCTGC	CTGTTGATCT	ACTGCCTGTG	AATTGCTTAT	CAAACCAACA	ACCAACTGGA	1380
ATACATAGAC	TGCATGTCTT	GTTCAATTTCC	TGCATTCTCA	AGTAATGGTT	TAACAAACTC	1440
ATGAGCTTAC	TCTTTAATCT	GAACCATGCT	TAACCTCAAT	TATGTTGATT	TAGTCTAAGG	1500
ATGCAGAATT	TATTTTATAG	TTATGTAGGA	ACTGGAATCC	AAAATGTAAT	ATGCCTCCAA	1560
GCTTTTCTTT	GTTGGCCTCT	GAAGGAGCAT	CACCTCTACA	ACTTCAACGT	TGTTATGAAT	1620
ACCTCTGGGG	AGGTGTTTAC	CTCAGGACCC	AAATTTGGAA	AAAGGGAAGT	GCCACTTTGG	1680
AGGAGTGCTC	TGAGCAGCTG	ATCCATTAAA	TGTC <sup>1</sup> CCGATC	ACATGCACGT	GGAAGTGTC	1740
TTGCAATATC	TGCACTAACA	GAAGCTCAGT	GACTTGAGAA	GTGAGTCTGG	AATTCTAAGA	1800
AAAAGGCAAG	GCATCTCTCT	TGCCACTTGT	TATTTTTCCT	GTCAAGCAAC	TGTGATAAGA	1860
GGGCATGGAG	AGCAGGAAGA	AGTGAAAAAT	CCCAGGAAAG	TCTGGAGTGG	AATCATTAATA	1920
CCAATTCTGC	TCCCTCTCTA	GGCCAACTTG	GGCCTATTAT	GAATAAGGAG	GTCTCTTATA	1980
ATCCATCTAA	CTCCACTCAG	GAACAATTTG	GGGATCTGAG	ACTGTGAACT	CAGTGGGCAA	2040
AAAAATATTT	CTTGGCCTAT	CATTATTCTC	TGTAGGATGT	TAAGGACAGG	TTTCTGTATG	2100
TGGAGTCCTC	AGTTTTTGCC	TTCTCTCCTT	GAGATATTTT	TATGCTATTT	AGTAATTGAT	2160
GGCCACAGTT	GATCGACCAC	ATTTCTGGGC	AACTCTAATA	ATCCTTGTTA	TATTAATCAT	2220
TGGACCAATC	TTGATTGTGT	ATGACCATCA	TCTTGATAGT	ACCACCTCTA	TGTGGATGCT	2280
CTCCTCACCC	TGCTTAAGTG	CCAATGTCTG	TGCTATGGGC	CTACCTGTCA	CATGGATAAT	2340
CTCTTCACTC	CAGTCAGGCT	CCAACATTAA	CACAGGGCTG	TTCTCTTGTC	CCCCTTTGAA	2400
GACAGCTTCA	TCACCTTATT	CAAGTTGCAG	TACTCTCACT	GGGCCTCCAC	TGTTGCCTCT	2460
CTCTCACTCT	GCTTAGGTTT	CTTCACTCCA	CTCCAGGCAA	CTGTCACTAA	ACATCCTTTC	2520
CCCCATATAT	AACACAGACA	TCTACCTTGC	TTGGCCAAAC	CCACTGGATT	TCAGACTCAC	2580
TCATTCAGAG	AGTAAGACAG	AGAGGGGTTC	ATTTTTTATT	TTATTTTATT	TTTTATTTTT	2640

TGAGACGTTG	TCTCACCTG	TCGCCCAGGC	TGGAGTGCAG	TGGTGCAGTC	TTGGCTCACT	2700
GCAATCCCCA	CGTCCCAGGT	TCAAACGATT	CTCCTGCCTC	AGTCTCCCAA	GCAGCTGGGA	2760
TTACAGGTGC	CTGCCACCAT	GCCCAGCTAA	TTTTTGTATT	TTAGTAGAG	ACAGGGTTTC	2820
GCCGTGTTGG	CCAGGCTGGT	CTCGAACTCC	TGACCTCAAG	TGATCTACCC	GCCTCGGCCT	2880
CCCAAAGTGC	TGGGATTACA	GGTGTGAGCC	ACTGCGCCCA	GCCGGGGTTC	ATCCTTAATA	2940
CATACATTAG	AGATATAGAT	TCTGTTTTTA	TCTAAAAAGT	CTTTATAAGG	CCGGGCGCGG	3000
TGGCTCACGC	CTGTAATCCC	AGCACTTTGG	GAGGCCGAGG	CGGGCGGATC	ACGAGGTCAG	3060
GAGATCGAGA	CCATCCCGGC	TAAAACGGTG	AAACCCCGTC	TCTACTAAAA	ATACAAAAAA	3120
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GCCTGGGCGA	CAGAGCAAGA	CTCCGTCTCA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAGT	3300
CTTTATAAAA	ATCTGATTGA	ATGGTTGAAT	GCTGTGCTAA	AATCTGCATA	ATATCTTACA	3360
ACACTTCTGT	GAATCACGAG	ACAGTTTTGA	ATGCTAAATG	TCAGTTAACA	GATCTAAAGG	3420
GACCAACATC	TGCTTTCCCA	AATTATATGA	AAGAAGATCC	TGATCCCTCA	TCAGGTGAAA	3480
CTCACATCAG	ACAACAGTGT	CTGCATTTCT	CCAAAACCCG	CCTCAGCCCC	ATGGCCACTT	3540
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GCCCTCAGTC	TTCTTGCTC	TGCTCTCCTT	CACAGCAGGC	TTTACCCCCC	ATGCTGGTCA	3840
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GGAGATCAAG	GAATGCCTTT	CCAGAAAAC	CCCCCTTATG	TCTCATTTGC	CAAAACTTGG	3960
CCTAGTCTCA	GGTGCTGCCT	GAGCTAATCA	GCTACAGAAG	AAGGGACCAC	ATGACTGGTG	4020
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GGGTGGATCA	CTTGAGGTCA	GGGGTTTGAG	ACCCGCCTGG	CCAACATGGT	TAAAACCTAT	240600
CTCTACTAAA	AATACAACGA	TTAGCCATGC	ATGGTGGCAC	ATGCCTGTAA	TCCCAGCTAC	240660
TCGGTAGCCT	GAGGCAGGAG	AATAGCTTGA	ACCCAAGAGG	CAGAGGTTAC	AGTGAGCCGA	240720

GATCGCACCA	CTCCAGCCTG	GGCAACAGAG	TGAGACTCCA	TCTCAAAACA	AAACAAAAAA	240780
ACTACTCAA	ACTGTAATA	GAAAAA	AACCTAATTA	TACATGTAAA	ACATTTAAAT	240840
AACTAAAATA	AGAATACTGT	TGACATAGTG	AGACATCCAT	TTATACTATG	GAATGTTATG	240900
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TAGAGAACCG	TATGGAAGAA	AACATACCAC	AGTAATTATC	TCAGATAGCT	GAAACTAAGT	241020
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GGGTCTAGGG	TTAATAGATG	TTTGCTTAAA	ATCATGGAAA	GAAAATGGTC	ACACAGCTGG	241800
TATGTGTGAT	CAAATTTGTG	CTGTTTCATC	CACTTAATGT	TTACTTTGTG	GTAATGGAAC	241860
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TCCTCCCTCC	CTCCCTCCCT	CCCTCCCTTC	CTTCTTTTCT	TCACAGAGTC	TAGCTCTGTT	241980
GCCCAGGCTG	GAATGCAGTG	GTGCGATCTC	AGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	242040
AAGCGATTCT	CCTGCCTCAG	CCTCCCAAGT	ATCTAGGATT	ACAGGTGCAT	GCTGCCACAC	242100
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ACTCTTACCT	GCTAGGATAA	GTTTGTGGA	GAATTTTACC	TTACCTTGTA	CCCTTTACCT	242340
TCACATCTAC	CTGTACCCTG	GCCCTTCACA	TCCTTTCCAT	ATAATATATC	TTCAGTAAAT	242400
ACAGGGAAAA	AAACCCAGAA	TGATTATGTT	GACAGCAAAA	CATGTTTGTG	CAGAAACGGA	242460
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TAAGTCAAAA	ATTCAGTTTC	CTCAGTCTCA	CCACATTTCA	GGTTGCTGGT	GTCTACTGTA	242700
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AGAAGTACTT	TGCCCAGGTA	CTGTGGCTTA	GGCCAGTAAT	CCTAGCATTT	GGGGAAGCCA	244800
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CCATCTCTAC	AAAATATGTA	AAATTTAACT	GCTTGGTGGG	CCTGCACTTC	TGGTCCCAGC	244920
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ATGATCACAG	CAATGCGCTC	CAGCTCTGGG	CAACAGAGCG	AGACCCTGTC	TCAAAAAAAAA	245040
CAAAAATGCC	TATACAATAA	ATCTATAAAA	AGTGGGTTTT	GTGTGTCTAT	ACACACACAC	245100
ACACACACAC	ACCTGCATAG	ACACTCAGGT	GTTCTGGAAA	GACACAGGAA	TCTGAAGCCA	245160
AAATACTTGT	GATTTTTTTT	CAGCTCTGCC	ACTCACCAAA	TGTCTGATGG	GATTAGTTAC	245220
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AAACTATCAA	ATGAGATGGC	AGATGAGAAA	ACACTATATT	CCTTGTAATA	CCTGACAAAT	245340
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TACCCACACA	CCTCCCACCA	AGTCAGCTCC	AGGTTTCAAG	GCAGCAGCCC	CAGTGGAAGG	245640
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AATGGTCACA	AAAACAAGTC	AATGGCTTTT	CCACATCCGT	ACATTGAGAT	ATATTTCTGC	246000
CCTTGGTATT	CATTTTCTCT	GACCTCCAAT	TAAAGATCTA	TGCGTCATTT	TAAAGCCTTC	246060
CTTCCTTTCT	ACTCTGTGGT	CAGCGTAACA	TTGGTGGTTT	GAAACTGGCC	ATAATAGCAG	246120
CATTTACATC	ATGGGAACCT	GCATATGTTA	CATCAGGGTT	TTTTTGTTTT	GTTTCTGGAG	246180
AGCCAGTAAA	CATACATCGT	CACACCACTT	AAATATTCTC	TGCTTAAATA	TTCTCTGCTC	246240

(2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..246240
- (D) OTHER INFORMATION: /note= "HLA-H.CONTIG"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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GCTGCACTTA TTTTATACAT TTTATTTATG TTAATAATCT CACATTTAAC ACACTTATGA	180
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ATATGTATAC TAGTTTCTCC ATCGATTCTT TAGATTTGAA ACTTATTTTC CTTTATTCTT	360
TACAAAACCTG ACTTGTCTAT AGGCCCACTT CTACTTCCTT TATTCTATCA TCTTCCTCAA	420
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CTTCCACCTG TTCTCTGAGA AATTCAGCTT CAAGAACTTT AGTTTGATAT GACTGCAAAG	540
ATAATACACA GTCTAAATCA TAAAAATGTC TCAAAGGTTT TTTTTTTATT TGTTTCTTTG	600
AAATATCCAT GAACAGGCAT GTTTCTCCCC CTGTAGTGCA ATTTGTGTGA AATTCTGGCA	660
TGCACTTAAG AGGATGTCCT AAAATACCAA TATTTAATTG ATTCTAAGTC ATGTATTGTA	720
TCACATTTTT GCCCATGGAT TGTTGAAATC CATGGACAAA ACTGATAGCA TTTTAGAACT	780
TCCTTTGTCT AGTGGCAGTC TTGATATATT CACACTATCT ATTGACAAAA AATCTAAAGC	840
ACCAGGCTCA AAGCTTGTAG AGTAGGTGTC AGTGATTGG AGGACATCTC TAGGGCAATA	900
GTAGAGGCAT TTTTAACCCC TAACAACATA ATGATCATCA GAAGTGAGTG ATATCCTCAC	960
TCATGACCCC AACTGCTCTA ATTTCTATTG TTTTCTTGCA GAAATGAGAG CAGGTGGGGT	1020
CATGGGTGAG GAATGAGGTG TTGAAAGTGA ATGGGGTGTT GAAAGCAAGG TGTTTAGCAG	1080
TGTTCTGAAA GCATACATTT AAGTAGGCTA TCCGGGCACT GTCAATAGCT AAGTGTCAG	1140
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AGATTTTCAA AGAGCCATCT AAGTTTCCAA AATAAGTGTT GCAGTCATAT TAACTATTAT	1320
ATTTTCCTGC CTGTTGATCT ACTGCCTGTG AATTGCTTAT CAAACCAACA ACCAACTGGA	1380

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CCAATTCTGC	TCCCTCTCTA	GGCCAACCTG	GGCCTATTAT	GAATAAGGAG	GTCTCTTATA	1980
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TGGAGTCCTC	AGTTTTTTGCC	TTCTCTCCTT	GAGATATTTT	TATGCTATTT	AGTAATTGAT	2160
GGCCACAGTT	GATCGACCAC	ATTTCTGGGC	AACTCTAATA	ATCCTTGTTA	TATTAATCAT	2220
TGGACCAATC	TTGATTGTGT	ATGACCATCA	TCTTGTAGCT	ACCACCTCTA	TGTGGATGCT	2280
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GCAATCCCCA	CGTCCCAGGT	TCAAACGATT	CTCCTGCCTC	AGTCTCCCAA	GCAGCTGGGA	2760
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TGGCTCACGC	CTGTAATCCC	AGCACTTTGG	GAGGCCGAGG	CGGGCGGATC	ACGAGGTCAG	3060
GAGATCGAGA	CCATCCCGGC	TAAAACGGTG	AAACCCCGTC	TCTACTAAAA	ATACAAAAAA	3120
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ACACTTCTGT	GAATCACGAG	ACAGTTTTGA	ATGCTAAATG	TCAGTTAACA	GATCTAAAGG	3420
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CCTAGTCTCA	GGTGCTGCCT	GAGCTAATCA	GCTACAGAAG	AAGGGACCAC	ATGACTGGTG	4020
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GCTGTGCACA	TCCACATACA	GGAATAGAAA	CTGATTCACA	CAAGTGCCAG	TAATGACTAT	32700
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AGAAGTACTT	TGCCCAGGTA	CTGTGGCTTA	GGCCAGTAAT	CCTAGCATTT	GGGGAAGCCA	244800
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CCATCTCTAC	AAAATATGTA	AAATTTAACT	GCTTGGTGGG	CCTGCACTTC	TGGTCCCAGC	244920
TACTCCAGGG	CTAGGGTGGG	AGGATTGTTT	GATCCCTGGA	GGTCAAGGCT	GCAGTGAGCC	244980
ATGATCACAG	CAATGCGCTC	CAGCTCTGGG	CAACAGAGCG	AGACCCTGTC	TCAAAAAAAA	245040

CAAAAATGCC TATACAATAA ATCTATAAAA AGTGGGTTTT GTGTGTCTAT ACACACACAC 245100  
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 AAATACTTGT GATTTTTTTTT CAGCTCTGCC ACTCACCAAA TGTCTGATGG GATTAGTTAC 245220  
 CTGCCATCTC AGAATTTCTC TTCTGTAAAA TAAGGTAATA GTACCTCCCA GAGTTATGAA 245280  
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 ACATGAAGCT TTTAGAAGAG TCAGCATGGT AGACATGGAA TGTTGAATGG TGGTGGAGTG 245580  
 TACCCACACA CCTCCCACCA AGTCAGCTCC AGGTTTCAGAA GCAGCAGCCC CAGTGGGAAGG 245640  
 CATGCGTGTT TGTAAGTCAG CTGAGCCACC TTTCAAGAAG CAGAAGCTTT CCAAACAGGG 245700  
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 GCACAGTCCC TTCAGATTAA GGATGAAGAG GCTGGGGTTC TGAATTGGTT GGCCTTAGGT 245940  
 AATGGTCACA AAAACAAGTC AATGGCTTTT CCACATCCGT ACATTGAGAT ATATTTCTGC 246000  
 CCTTGGTATT CATTTTCTCT GACCTCCAAT TAAAGATCTA TGCCTCATTT TAAAGCCTTC 246060  
 CTTCTTTTCT ACTCTGTGGT CAGCGTAACA TTGGTGGTTT GAAACTGGCC ATAATAGCAG 246120  
 CATTTACATC ATGGGAAC TA GCATATGTTA CATCAGGTT TTTTGT TTTT GTTTCTGGAG 246180  
 AGCCAGTAAA CATAATCGT CACACCACTT AAATATTCTC TGCTTAAATA TTCTCTGCTC 246240

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..246240
- (D) OTHER INFORMATION: /note= "HLA-H.CONTIG"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTGTAAGTA TTCTATTTTA TTTATATGTG TTTGTGTTTC TGAGTATGTC CTGAGTTGCA 60  
 CGATAATACT ATATTTCTTA TTGGGTAACA TTGTCAGAAA AGTTTCTAAA AACTTTCTCT 120

GCTGCACTTA	TTTTATACAT	TTTATTTATG	TTAATAATCT	CACATTTAAC	ACACTTATGA	180
TTTATTCTCA	ACAGAAAAAG	GTGGTATTTT	TTTCATTTAG	TCTTTTAAAA	AGCTCACATT	240
ATCAAATGAT	TGCTCAATCA	TTTAATCTCT	TTGCTTCTCT	TATATGCATT	GATTTAATAA	300
ATATGTATAC	TAGTTTCTCC	ATCGATTCTT	TAGATTTGAA	ACTTATTTTC	CTTTTATTCT	360
TACAAAACTG	ACTTGTCTAT	AGGCCCACTT	CTACTTCCTT	TATTCTATCA	TCTTCCTCAA	420
CTTATTCTGT	GGTCAAAGAA	TGGAGAAATA	ATATTAATAA	TATGTTTTTC	TCATCAATGA	480
CTTCCACCTG	TTCTCTGAGA	AATTCAGCTT	CAAGAACTTT	AGTTTGATAT	GACTGCAAAG	540
ATAATACACA	GTCTAAATCA	TAAAAATGTC	TCAAAGGTTT	TTTTTTTATT	TGTTTCTTTG	600
AAATATCCAT	GAACAGGCAT	GTTTCTCCCC	CTGTAGTGCA	ATTTGTGTGA	AATTCTGGCA	660
TGCACTTAAG	AGGATGTCCT	AAAATACCAA	TATTTAATTG	ATTCTAAGTC	ATGTATTGTA	720
TCACATTTTT	GCCCATGGAT	TGTTGAAATC	CATGGACAAA	ACTGATAGCA	TTTTAGAACT	780
TCCTTTGTCT	AGTGGCAGTC	TTGATATATT	CACACTATCT	ATTGACAAAA	AATCTAAAGC	840
ACCAGGCTCA	AAGCTTG TAG	AGTAGGTGTC	AGTGATTGG	AGGACATCTC	TAGGGCAATA	900
GTAGAGGCAT	TTTTAACCCC	TAACAACTAA	ATGATCATCA	GAAGTGAGTG	ATATCCTCAC	960
TCATGACCCC	AAC TGCTCTA	ATTTCTATTG	TTTTCTTGCA	GAAATGAGAG	CAGGTGGGGT	1020
CATGGGTGAG	GAATGAGGTG	TTGAAAGTGA	ATGGGGTGTT	GAAAGCAAAG	TGTTTAGCAG	1080
TGTTCTGAAA	GCATACATTT	AAGTAGGCTA	TCCGGGCACT	GTCAATAGCT	AAGTGCAAG	1140
CTAAGTACTC	TATTTTATTC	TAAGAACTAT	TTTTAGAAAT	GCTGAATCAA	CAAATCTCAG	1200
ATGGCACAGA	GGTTGTCATT	TTTGAATAAT	ATGAATATCA	GTAATTTTAG	TTGGAAAAGA	1260
AGATTTTCAA	AGAGCCATCT	AAGTTTCCAA	AATAAGTGTT	GCAGTCATAT	TAAC TATTAT	1320
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ATGAGCTTAC	TCTTTAATCT	GAACCATGCT	TAAC TTCAAT	TATGTTGATT	TAGTCTAAGG	1500
ATGCAGAATT	TATTTTATAG	TTATGTAGGA	ACTGGAATCC	AAAATGTAAT	ATGCCTCCAA	1560
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CCAATTCTGC	TCCCTCTCTA	GGCCA ACTTG	GGCCTATTAT	GAATAAGGAG	GTCTCTTATA	1980

ATCCATCTAA	CTCCACTCAG	GAACAATTTG	GGGATCTGAG	ACTGTGAACT	CAGTGGGCAA	2040
AAAAATATTT	CTTGGCCTAT	CATTATTCTC	TGTAGGATGT	TAAGGACAGG	TTTCTGTATG	2100
TGGAGTCCTC	AGTTTTTGCC	TTCTCTCCTT	GAGATATTTT	TATGCTATTT	AGTAATTGAT	2160
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CCCCATATAT	AACACAGACA	TCTACCTTGC	TTGGCCAAAC	CCACTGGATT	TCAGACTCAC	2580
TCATTCAGAG	AGTAAGACAG	AGAGGGGTTC	ATTTTTTATT	TTATTTTATT	TTTTATTTTT	2640
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GCAATCCCCA	CGTCCCAGGT	TCAAACGATT	CTCCTGCCTC	AGTCTCCCAA	GCAGCTGGGA	2760
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GCCGTGTTGG	CCAGGCTGGT	CTCGAACTCC	TGACCTCAAG	TGATCTACCC	GCCTCGGCCT	2880
CCCAAAGTGC	TGGGATTACA	GGTGTGAGCC	ACTGCGCCCA	GCCGGGGTTC	ATCCTTAATA	2940
CATACATTAG	AGATATAGAT	TCTGTTTTTA	TCTAAAAAGT	CTTTATAAGG	CCGGGCGCGG	3000
TGGCTCACGC	CTGTAATCCC	AGCACTTTGG	GAGGCCGAGG	CGGGCGGATC	ACGAGGTCAG	3060
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TTAGCCGGGC	GTAGTGCGCG	GCGCCTGTAG	TCCCAGCTAC	TTGGGAGGCT	GAGGCAGGAG	3180
AATGGCGTGA	ACCCGGGAGG	CGGAGCTTGC	AGTGAGCCGA	GATCCCGCCA	CTGCACTCCA	3240
GCCTGGGCGA	CAGAGCAAGA	CTCCGTCTCA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAGT	3300
CTTTATAAAA	ATCTGATTGA	ATGGTTGAAT	GCTGTGCTAA	AATCTGCATA	ATATCTTACA	3360
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AAACAGGACA	TCAAAGGCAG	AAAGGTTCCT	GAGCAGGGTG	ATCAGAGCTC	TGGCTCCACT	3780
GCCCTCAGTC	TTCTTGCTC	TGCTCTCCTT	CACAGCAGGC	TTTACCCCCC	ATGCTGGTCA	3840

CAGTTTCAAG	TGTCCATGCA	GACACAAGTT	AAAGGCAGGA	AGAAACAGTG	CGTTTCTCTT	3900
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TGGACCAGTC	AGAATTCACC	ACATGAAGCT	AGTAATGTGG	CTCACACTTC	CCAGGGGGAT	4080
ATGGCCAGGT	AGCAGACAGT	GGATCGCTGA	ACAGAATACT	GATAGATTTC	AGCACCAAGG	4140
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CTCAGTCACA	ATCATTTTTT	GATAGCCTAT	CCTATAAGCT	TAACCTATAG	TGTTAATCAG	4380
TATTAATACA	TCTTAGTGGG	AAAGAAGGAA	AAAATAAACG	ATCACACACA	CACACACACA	4440
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GCTCACAAAC	ACAGCCAGAA	ATAATGTTTA	ACCAGATAGC	TGGTTATCCC	CTGACTCAGT	5520
CAAGTTGACA	CAAAAAATGA	ACTATTTCAA	AGCTTACTGT	AATCAACAGT	TTTGTCAAAA	5580
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AGTGGTGAAA	TCCACATAAA	GTCTAGGGTT	TGGTTAATAG	AGTTTCATGT	ATCAATGTGA	6360
GTTGCTTATA	TTTGACAAAT	GTATCATAAT	AATGTAAAAAT	CCTAACAATG	GGGGAAAGCT	6420
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GAGTATCCCT	TATGCTTAGA	ACCAGAAGTA	TTTCAGATTT	TTTCAGATTT	GGAATGTTTG	6660
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TGCTGTGTTT	AACTAGGGCT	CTTGATAATC	TGACCAGCTT	CTGTCTTACT	GATTTTAGGA		9240
GAAAAATGGA	GCAACCTGCA	AGATGAGTGG	GATTAGCTTC	GTGCTGTCTC	CCATGCACAC		9300
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GCCTTGACTA	CATGTTCCCA	CCCCACCCCT	ATCCCATCTG	TACTCTCTGA	GTCTGACATC	236460
AAAGTGGCAG	CCCTGGCGGC	TCCTGCCTGT	AATCCCAGCA	CTTTGGGAGG	CCAATGAGAA	236520
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TACTAAAAAT	ACAAAAATTA	GCTGGGCAAG	TGGTGGCAGG	AGCGCTACTC	GGGAGGGTAC	236640
AGATTTAGAG	CCTGTAATCC	CAGCTACTTG	GGAGTCTAAG	GCAAGAGAAT	CCCTTGAACC	236700
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TGAGACTGCC	TCAAGAAAAA	ACAAAAGAGT	CAGCCCTAGT	GATCTTGTA	GTTGCCTTTG	236820
GTGGGTCAGT	CTTTCCTTTT	CTTAAAGAAT	AGTACACATT	GACAGCCAGG	TAGCTCTATG	236880
ATCCTGTTCT	ATAGAATTCA	AAAAGTCGAC	AACCTTCCTT	TGTTCCCTTC	TGTTTTCTCT	236940
GCCTACGTTA	GTTTAAATTG	GCAGTGTCTC	TGCTGGAATA	ATCCCATCTC	TCTTCCTGGC	237000
TTCTGCTGAG	ATGGCTGATT	AAATCCTTGG	GTCACACCCA	TTATCTCTTT	ATCAAATGGT	237060
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GGCAGATCAC	TTGAGCTCAG	GAGTTAGAGA	CCAGCCTAGG	CAACATGTCA	AAACCCCATC	237180
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CACTTTAAGC	AGTAAGGAGG	ACCTAAATCA	CACCTTCAAT	ACTTTGCTTA	GACATCTCTT	237600
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CAGCCAAGTT	CTTGACACAT	TGTAACAAGA	ACAGTGATTT	CTACAGTTTC	CAATAACCTG	237720
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TTAGTAGAGA	CAGGGTTTCG	CCATATTGGC	CAGGCTGGTC	TCAAACCTCC	GACCTCGTGA	238020
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ACTCATCAGG	TCCCAGCTCT	GTTTCAGACA	AGGCTATCTA	AAATAGACCT	ACCTAAATGG	239340
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ATACCTCATT	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTTTG	GAAATGGTGA	239460
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ACCTTCCTAG	TAATTCAAAA	TTATGCATAT	TAATACAACA	AAGGGATACC	ACTTCTTTTT	239820
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TCTCAACTCA	CTGCAACTTC	CACCCCTTGG	GTTCAAGCGA	TTCTCCTGCC	TCAGCCTCCC	239940
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TCCTGACCTC	AGATGATCCA	CCCACTTCAG	GCTCCCAAAG	TGCTGGGATT	ACAGGCATGA	240240
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CAGTTTGAAG	TTTTATTTAT	GAGATTCCTT	GTTGTTTGCC	TCTTTCCATT	AAACCTAGCT	241320
CCACAAAGTA	GGGACCTGAT	GTATTCATTC	ACTGTTATAT	CCCAGCATCT	AGCAGAGGGC	241380
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CAACACCAGG	CCTCAAGTGA	TCCGCCTGCC	TTGGCCTCCC	AAATTGCTGG	GATTAACAGG	242220
CCTCAGCCAC	TGTGCCCCGAC	CCCAGCTTTT	ATATTCTAAT	GCTGAGATTA	TTCAGTTAAC	242280
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TACCCACACA	CCTCCCACCA	AGTCAGCTCC	AGGTTTCAGAA	GCAGCAGCCC	CAGTGGAAGG	245640

CATGCGTGTT TGTAAGTCAG CTGAGCCACC TTTCAAGAAG CAGAAGCTTT CCAAACAGGG 245700  
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 CATTTACATC ATGGGAACATA GCATATGTTA CATCAGGGTT TTTTGTGTTT GTTTCTGGAG 246180  
 AGCCAGTAAA CATAATCGT CACACCACTT AAATATTCTC TGCTTAAATA TTCTCTGCTC 246240

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Mbo I-S primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCTGATGCTC GAGTGAATTC

20

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "vector-vector splicing"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGACCCAGCA ACCTGGAGAT

20



## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "cryptic donor-1021"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGCTCGAGCG GCCGCTGCAG

20

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "cryptic donor-1134"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGACCCCAAC CCACAAGAAG

20

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "MAP1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGTTAGAACG CGGCTACAAT

20

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..20
  - (D) OTHER INFORMATION: /note= "MAP2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCCGATTCAT TAATGCAGGT

20

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..20
  - (D) OTHER INFORMATION: /note= "-21"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTGTAAAACG ACGGCCAGTC

20

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..19
  - (D) OTHER INFORMATION: /note= "REV"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCAGGAAACA GCTATGACC

19

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "may be I or V"

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "X is 11-30 peptides long"

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "may be F, I or L"

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "may be I, L or M"

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "X is 10-18 peptides long"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Cys Xaa Xaa Cys Xaa Cys Xaa His Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa  
 1 5 10 15

Cys Pro Xaa Cys  
 20